

STIC-Biotech/ChemLib

From: Hashemi, Shar
Sent: Monday, August 19, 2002 11:21 PM
To: STIC-Biotech/ChemLib
Subject: Please search ALL NA including Pending SEQ. ID NO: 9, 29-31, 33 (five sequences) for application 10/077,383

Please search ALL NA including Pending SEQ. ID NO: 9, 29-31, 33 (five sequences) for application 10/077,383

Thanks,
Examiner Hashemi
CM1 12D04
703-305-4840

Shar,

The seqs. disclosed for
Seq. IDs 9, 30 & 33 consists
only of "N"s; therefore, no
query match > 0 was
located/retrieved.

Beverly
1E05
C8-4994

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

1

2

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: <u>08-26-02</u>	Search Site	Vendors
Searcher: <u>Beverly E 499A</u>	<input type="checkbox"/> STIC	<input type="checkbox"/> IG
Terminal time: <u>20</u>	<input type="checkbox"/> CM-1	<input type="checkbox"/> STN
Elapsed time: _____	<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input type="checkbox"/> APS
Total time: <u>28</u>	<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
Number of Searches: _____	<input type="checkbox"/> A.A. Sequence	<input type="checkbox"/> SDC
Number of Databases: <u>1</u>	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>CGN</u>

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and the role of the accounting system in providing reliable financial information. It emphasizes the need for transparency and accountability in financial reporting.

2. The second part of the document outlines the various methods used to collect and analyze financial data, including the use of statistical techniques and the application of mathematical models. It highlights the importance of using appropriate methods to ensure the accuracy and reliability of the results.

3. The third part of the document discusses the challenges faced by organizations in managing their financial resources effectively. It identifies key areas such as budgeting, forecasting, and risk management, and provides strategies to address these challenges.

4. The fourth part of the document focuses on the role of the accounting system in providing timely and accurate financial information to management and stakeholders. It discusses the importance of maintaining up-to-date records and the use of modern accounting software to streamline the process.

5. The fifth part of the document discusses the importance of maintaining accurate records of all transactions and the role of the accounting system in providing reliable financial information. It emphasizes the need for transparency and accountability in financial reporting.

6. The sixth part of the document outlines the various methods used to collect and analyze financial data, including the use of statistical techniques and the application of mathematical models. It highlights the importance of using appropriate methods to ensure the accuracy and reliability of the results.

7. The seventh part of the document discusses the challenges faced by organizations in managing their financial resources effectively. It identifies key areas such as budgeting, forecasting, and risk management, and provides strategies to address these challenges.

8. The eighth part of the document focuses on the role of the accounting system in providing timely and accurate financial information to management and stakeholders. It discusses the importance of maintaining up-to-date records and the use of modern accounting software to streamline the process.

9. The ninth part of the document discusses the importance of maintaining accurate records of all transactions and the role of the accounting system in providing reliable financial information. It emphasizes the need for transparency and accountability in financial reporting.

10. The tenth part of the document outlines the various methods used to collect and analyze financial data, including the use of statistical techniques and the application of mathematical models. It highlights the importance of using appropriate methods to ensure the accuracy and reliability of the results.

c 32 0 0.0 1 24 US-09-625-102-614 Sequence 614, App
c 33 0 0.0 1 24 US-09-625-102-836 Sequence 836, App
c 34 0 0.0 1 24 US-09-625-102-836 Sequence 836, App
c 35 0 0.0 1 24 US-09-625-102-895 Sequence 895, App
c 36 0 0.0 1 24 US-09-625-102-895 Sequence 895, App
c 37 0 0.0 1 24 US-09-625-102-895 Sequence 895, App
c 38 0 0.0 1 24 US-09-625-102-895 Sequence 895, App
c 39 0 0.0 1 24 US-09-625-102-895 Sequence 895, App
c 40 0 0.0 1 24 US-09-625-102-1048 Sequence 1048, App
c 41 0 0.0 1 24 US-09-625-102-1048 Sequence 1048, App
c 42 0 0.0 1 24 US-09-625-102-1352 Sequence 1352, App
c 43 0 0.0 1 24 US-09-625-102-1352 Sequence 1352, App
c 44 0 0.0 1 24 US-09-634-306B-51773 Sequence 51773, A
c 45 0 0.0 1 24 US-09-634-306B-51773 Sequence 51773, A
Sequence 51841, A

ALIGNMENTS

RESULT 1
PCT-US93-00977-702
; Sequence 702, Application PC/TUS9300977
; GENERAL INFORMATION:
; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
; NUMBER OF SEQUENCES: 711
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson, and Bear
; STREET: 620 Newport Center Dr. Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00977
; FILING DATE: 19930129
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: HITACHI.006H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 702:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-00977-702

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 A 1

RESULT 2
PCT-US93-00977-702/c
; Sequence 702, Application PC/TUS9300977
; GENERAL INFORMATION:
; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
; NUMBER OF SEQUENCES: 711
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson, and Bear
; STREET: 620 Newport Center Dr. Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00977
; FILING DATE: 19930129
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: HITACHI.006H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 702:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-00977-702

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 A 1

RESULT 3
US-08-068-298-17
; Sequence 17, Application US/08068298
; GENERAL INFORMATION:
; APPLICANT: MUENCHAU, DARYL, ET AL.
; TITLE OF INVENTION: METHOD FOR GENERATING APTAMERS OF
; TITLE OF INVENTION: NON-PREDETERMINED OR SUBSTANTIALLY
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 611 West Sixth St.
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,298
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/659,980

; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
; NUMBER OF SEQUENCES: 711
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson, and Bear
; STREET: 620 Newport Center Dr. Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00977
; FILING DATE: 19930129
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: HITACHI.006H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 702:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-00977-702

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 T 1

RESULT 3
US-08-068-298-17
; Sequence 17, Application US/08068298
; GENERAL INFORMATION:
; APPLICANT: MUENCHAU, DARYL, ET AL.
; TITLE OF INVENTION: METHOD FOR GENERATING APTAMERS OF
; TITLE OF INVENTION: NON-PREDETERMINED OR SUBSTANTIALLY
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 611 West Sixth St.
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,298
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/659,980

; FILING DATE: February 21, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CONSALVI, MARY S
; REGISTRATION NUMBER: 32,212
; REFERENCE/DOCKET NUMBER: 193/051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; FEATURE:
; OTHER INFORMATION: where N also may be isoguanine or
; isocytostine
; US-08-068-298-17

Query Match 0.0%; Score 0; DB 4; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 G 1

RESULT 4
US-08-068-298-17/c
; Sequence 17, Application US/08068298
; GENERAL INFORMATION:
; APPLICANT: MUENCHAU, DARYL, ET AL.
; TITLE OF INVENTION: METHOD FOR GENERATING APTAMERS OF
; TITLE OF INVENTION: NON-PREDETERMINED OR SUBSTANTIALLY
; TITLE OF INVENTION: NON-PREDETERMINED SEQUENCES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 611 West Sixth St.
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,298
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/659,980
; FILING DATE: February 21, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CONSALVI, MARY S
; REGISTRATION NUMBER: 32,212
; REFERENCE/DOCKET NUMBER: 193/051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; FEATURE:

; OTHER INFORMATION: where N also may be isoguanine or
; isocytostine
; US-08-068-298-17

Query Match 0.0%; Score 0; DB 4; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 C 1

RESULT 5
US-08-154-792A-9
; Sequence 9, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.
; APPLICANT: Reenan, Robert A.G.
; APPLICANT: Fishel, Richard
; TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 A 1

RESULT 6
US-08-154-792A-9/c
; Sequence 9, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.

APPLICANT: Reenan, Robert A.G.
APPLICANT: Fishel, Richard
TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
and Uses Therefor
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: David G. Conlin, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,792A
FILING DATE: 17-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44824
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-154-792A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n l
Db 1 T l

RESULT 7
US-08-154-792A-24
Sequence 24, Application US/08154792A
GENERAL INFORMATION:
APPLICANT: Kolodner, Richard D.
APPLICANT: Reenan, Robert A.G.
APPLICANT: Fishel, Richard
TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
and Uses Therefor
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,792A
FILING DATE: 17-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44824
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-154-792A-24

APPLICATION NUMBER: US/08/154,792A
FILING DATE: 17-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44824
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-154-792A-24

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n l
Db 1 A l

RESULT 8
US-08-154-792A-24/c
Sequence 24, Application US/08154792A
GENERAL INFORMATION:
APPLICANT: Kolodner, Richard D.
APPLICANT: Reenan, Robert A.G.
APPLICANT: Fishel, Richard
TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
and Uses Therefor
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,792A
FILING DATE: 17-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44824
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-154-792A-24

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 T 1

RESULT 9
 US-08-163-449A-9
 ; Sequence 9, Application US/08163449A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kolodner, Richard D.
 ; APPLICANT: Reenan, Robert A.G.
 ; APPLICANT: Fishel, Richard
 ; TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 ; TITLE OF INVENTION: PRODUCTS, AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 44
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 ; ADDRESSEE: ROBERTS & CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/163,449A
 ; FILING DATE: 07-DEC-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Resnick, David S.
 ; REGISTRATION NUMBER: 34,234
 ; REFERENCE/DOCKET NUMBER: 44824-CIP-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 523-3400
 ; TELEFAX: (617) 523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 9:
 ; LENGTH: 1 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-163-449A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 A 1

RESULT 10
 US-08-163-449A-9/c
 ; Sequence 9, Application US/08163449A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kolodner, Richard D.
 ; APPLICANT: Reenan, Robert A.G.
 ; APPLICANT: Fishel, Richard

; TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 ; TITLE OF INVENTION: PRODUCTS, AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 ; ADDRESSEE: ROBERTS & CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/163,449A
 ; FILING DATE: 07-DEC-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Resnick, David S.
 ; REGISTRATION NUMBER: 34,234
 ; REFERENCE/DOCKET NUMBER: 44824-CIP-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 523-3400
 ; TELEFAX: (617) 523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 9:
 ; LENGTH: 1 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-163-449A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 T 1

RESULT 11
 US-08-163-449A-24
 ; Sequence 24, Application US/08163449A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kolodner, Richard D.
 ; APPLICANT: Reenan, Robert A.G.
 ; APPLICANT: Fishel, Richard
 ; TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 ; TITLE OF INVENTION: PRODUCTS, AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 ; ADDRESSEE: ROBERTS & CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/163,449A
 FILING DATE: 07-DEC-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,234
 REFERENCE/DOCKET NUMBER: 44824-CIP-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 523-3400
 TELEFAX: (617) 523-6440
 TELEX: 200291 STRE UR
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-163-449A-24

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 A 1

RESULT 12

US-08-163-449A-24/c
 Sequence 24, Application US/08163449A

GENERAL INFORMATION:
 APPLICANT: Kolodner, Richard D.
 APPLICANT: Reenan, Robert A.G.
 APPLICANT: Fishel, Richard
 TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 TITLE OF INVENTION: PRODUCTS
 TITLE OF INVENTION: AND USES THEREFOR
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/163,449A
 FILING DATE: 07-DEC-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,234
 REFERENCE/DOCKET NUMBER: 44824-CIP-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 523-3400
 TELEFAX: (617) 523-6440
 TELEX: 200291 STRE UR
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-08-163-449A-24

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 T 1

RESULT 13

US-08-208-572-10
 Sequence 10, Application US/08208572

GENERAL INFORMATION:
 APPLICANT: Silberstein Ph.D., David S.
 APPLICANT: Balcewicz-Sablinska M.D., Maria K.
 APPLICANT: Newman Ph.D., Gale W.
 TITLE OF INVENTION: CONTROL OF HIV GROWTH WITH ECEF AND
 DERIVATIVES
 TITLE OF INVENTION: ECEF
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CHORTE, HALL, & STEWART
 STREET: Exchange Place, 53 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/208,572
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Kaplan Esq., Warren A.
 REGISTRATION NUMBER: 34,199
 REFERENCE/DOCKET NUMBER: 092662-002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-5020
 TELEFAX: (617) 227-7566
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-208-572-10

Query Match 0.0%; Score 0; DB 6; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 A 1

RESULT 14

US-08-208-572-10/c

Sequence 10, Application US/08208572
 GENERAL INFORMATION:
 APPLICANT: Silberstein Ph.D., David S.
 APPLICANT: Balcewicz-Sablinska M.D., Maria K.
 APPLICANT: Newman Ph.D., Gale W.
 TITLE OF INVENTION: CONTROL OF HIV GROWTH WITH ECEF AND
 DERIVATIVES

```

; TITLE OF INVENTION: ECFE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHORATE, HALL, & STEWART
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,572
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan Esq., Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: 092662-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-5020
; TELEFAX: (617) 227-7566
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-208-572-10

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```

Query Match          0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 n 1
Db 1 T 1

```

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RESULT 15
US-08-237-491-6868
; Sequence 6868, Application US/08237491
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey
; APPLICANT: Delegeane, Angelo
; APPLICANT: Jernigan, Colleen
; APPLICANT: Levine, Wendy B.
; TITLE OF INVENTION: SHEAR-STRESSED HUMAN UMBILICAL VEIN
; TITLE OF INVENTION: ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 7326
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,491
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/137,951
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,801
; FILING DATE: 17-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8135-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6868:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: Z-068903
; US-08-237-491-6868

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```

Query Match          0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 n 1
Db 1 C 1

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Search completed: August 25, 2002, 00:32:24
Job time: 16382 sec

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; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51773
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51773

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 G 1

RESULT 3

US-10-027-632-51841
; Sequence 51841, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51841
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51841

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 Y 1

RESULT 4

US-10-027-632-51841/c
; Sequence 51841, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51841
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51841

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 R 1

RESULT 5

US-10-027-632-52001
; Sequence 52001, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52001
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52001

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 n 1
Db 1 y 1

RESULT 6

US-10-027-632-52001/c
; Sequence 52001, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52001
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52001

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 n 1
Db 1 r 1

RESULT 7

US-10-027-632-52051
; Sequence 52051, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52051
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52051

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

RESULT 8

US-10-027-632-52051/c
; Sequence 52051, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52051
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52051

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 g 1

RESULT 9

US-10-027-632-52156
; Sequence 52156, Application US/10027632
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52156
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52156

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

RESULT 10
US-10-027-632-52156/c
; Sequence 52156, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52156
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52156

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 n 1
Db 1 g 1

RESULT 11
US-10-027-632-52157
; Sequence 52157, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52157
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52157

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

RESULT 12
US-10-027-632-52157/c
; Sequence 52157, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52157
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52157

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 G 1

RESULT 13

US-10-027-632-52177
; Sequence 52177, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52177
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52177

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

RESULT 14

US-10-027-632-52177/c
; Sequence 52177, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52177
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52177

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 G 1

RESULT 15

US-10-027-632-52215
; Sequence 52215, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52215
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52215

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

Search completed: August 25, 2002, 00:45:45

Job time: 12372 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 00:32:24 ; Search time 8635 Seconds
(without alignments)
50.110 Million cell updates/sec

Title: US-10-077-383-29
Perfect score: 20
Sequence: 1 agagagagagagagagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 1081749327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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c 2	20	100.0	21	9	US-08-531-241A-807
c 3	20	100.0	21	16	US-09-263-959-807
c 4	20	100.0	22	26	US-09-669-187A-908
c 5	20	100.0	22	37	US-10-017-995-908
c 6	20	100.0	24	7	US-08-320-507-8
c 7	20	100.0	24	7	US-08-320-507-9
c 8	20	100.0	24	7	US-08-320-507-10
c 9	20	100.0	24	7	US-08-320-507-11
c 10	20	100.0	24	18	US-09-487-130-1
c 11	20	100.0	24	18	US-09-487-130-2
c 12	20	100.0	24	18	US-09-487-130-3
c 13	20	100.0	24	18	US-09-487-130-4
c 14	20	100.0	24	18	US-09-487-130-5
c 15	20	100.0	24	18	US-09-487-130-6
c 16	20	100.0	25	35	US-09-956-584-570432
c 17	20	100.0	25	62	US-60-234-017-532893
c 18	20	100.0	26	7	US-08-309-335A-538
c 19	20	100.0	26	9	US-08-531-241A-538
c 20	20	100.0	26	16	US-09-263-959-538
c 21	20	100.0	27	23	US-09-605-699-2355
c 22	20	100.0	27	29	US-09-735-363A-6
c 23	20	100.0	28	1	PCT-US98-07592-1
c 24	20	100.0	28	7	US-08-369-881-3317
c 25	20	100.0	28	8	US-08-842-872-1194
c 26	20	100.0	28	12	US-08-862-610-1
c 27	20	100.0	28	12	US-08-893-971-2
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45 20 100.0 41 4 US-08-055-985-66

Sequence 3, Appli
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Sequence 364, App
Sequence 60, Appl
Sequence 18866, A
Sequence 66, Appl
Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-08-309-335A-807/c
; Sequence 807, Application US/08309335A
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; APPLICANT: Rowen, Lee
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/309,335A
; FILING DATE: 19-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 240052.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 807:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-309-335A-807

Query Match 100.0%; Score 20; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agagagagagagagagagag 20
Db 21 AGAGAGAGAGAGAGAGAG 2

RESULT 2
US-08-531-241A-807/c
; Sequence 807, Application US/08531241A
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; APPLICANT: Rowen, Lee
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.

Query Match 100.0%; Score 20; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agagagagagagagagagag 20
Db 21 AGAGAGAGAGAGAGAGAG 2

RESULT 2
US-08-531-241A-807/c
; Sequence 807, Application US/08531241A
; GENERAL INFORMATION:

; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; APPLICANT: Rowen, Lee
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,241A
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 240052.406C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 807:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-531-241A-807

Query Match 100.0%; Score 20; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 AGAGAGAGAGAGAGAGAG 2

RESULT 3
US-09-263-959-807/c
; Sequence 807, Application US/09263959
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; APPLICANT: Rowen, Lee
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 807:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-807

Query Match 100.0%; Score 20; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 AGAGAGAGAGAGAGAGAG 2

RESULT 4

US-09-669-187A-908/C
SEQUENCE 908, Application US/09669187A
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Schetter, Christian
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/09/669,187A
PRIOR FILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: US 60/227,436
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1145
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 908
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-669-187A-908

Query Match 100.0%; Score 20; DB 26; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 AGAGAGAGAGAGAGAGAG 3

RESULT 5

US-10-017-995-908/c
SEQUENCE 908, Application US/10017995
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
FILE REFERENCE: C1037/7025 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,534
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 908
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-017-995-908

Query Match 100.0%; Score 20; DB 37; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 AGAGAGAGAGAGAGAGAG 3

RESULT 6

US-08-320-507-8
SEQUENCE 8, Application US/08320507
GENERAL INFORMATION:
APPLICANT: Gray
TITLE OF INVENTION: A method for ranking sequences to
TITLE OF INVENTION: select target sequence zones of nucleic acids.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Daniel F. Perez
STREET: 703 McKinney Ave., Suite 316
CITY: Dallas
STATE: Texas
COUNTRY: USA
ZIP: 75202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Dos 6.0
SOFTWARE: WordPerfect 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,507
FILING DATE: 07-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Perez, Daniel F
REGISTRATION NUMBER: 33,755
REFERENCE/DOCKET NUMBER: 1110-2012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (214) 871-1677
TELEFAX: (214) 817-1083
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-320-507-8

Query Match 100.0%; Score 20; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
Db 1 AGAGAGAGAGAGAGAGAG 20

RESULT 7

US-08-320-507-9/c
SEQUENCE 9, Application US/08320507

```
;
; GENERAL INFORMATION:
; APPLICANT: Gray
; TITLE OF INVENTION: A method for ranking sequences to
; select target sequence zones of nucleic acids.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Daniel F. Perez
; STREET: 703 McKinney Ave., Suite 316
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Dos 6.0
; SOFTWARE: Wordperfect 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,507
; FILING DATE: 07-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perez, Daniel F.
; REGISTRATION NUMBER: 33,755
; REFERENCE/DOCKET NUMBER: 1110-2012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 871-1677
; TELEFAX: (214) 817-1083
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-320-507-9
;
; Query Match 100.0%; Score 20; DB 7; Length 24;
; Best Local Similarity 100.0%; Pred. No. 7.4e+02;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 agagagagagagagagagag 20
; DB 24 AGAGAGAGAGAGAGAGAG 5
;
; RESULT 8
; US-08-320-507-10/c
; Sequence 10, Application US/08320507
; GENERAL INFORMATION:
; APPLICANT: Gray
; TITLE OF INVENTION: A method for ranking sequences to
; select target sequence zones of nucleic acids.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Daniel F. Perez
; STREET: 703 McKinney Ave., Suite 316
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Dos 6.0
; SOFTWARE: Wordperfect 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,507
; FILING DATE: 07-OCT-1994
; CLASSIFICATION: 435
;
; US-08-320-507-10/c
; Query Match 100.0%; Score 20; DB 7; Length 24;
; Best Local Similarity 100.0%; Pred. No. 7.4e+02;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 agagagagagagagagagag 20
; DB 24 AGAGAGAGAGAGAGAGAG 5
;
; RESULT 8
; US-08-320-507-10/c
; Sequence 10, Application US/08320507
; GENERAL INFORMATION:
; APPLICANT: Gray
; TITLE OF INVENTION: A method for ranking sequences to
; select target sequence zones of nucleic acids.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Daniel F. Perez
; STREET: 703 McKinney Ave., Suite 316
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Dos 6.0
; SOFTWARE: Wordperfect 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,507
; FILING DATE: 07-OCT-1994
; CLASSIFICATION: 435
```

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perez, Daniel F.
; REGISTRATION NUMBER: 33,755
; REFERENCE/DOCKET NUMBER: 1110-2012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 871-1677
; TELEFAX: (214) 817-1083
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-320-507-10
;
; Query Match 100.0%; Score 20; DB 7; Length 24;
; Best Local Similarity 100.0%; Pred. No. 7.4e+02;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 agagagagagagagagagag 20
; DB 23 AGAGAGAGAGAGAGAGAG 4
;
; RESULT 9
; US-08-320-507-11
; Sequence 11, Application US/08320507
; GENERAL INFORMATION:
; APPLICANT: Gray
; TITLE OF INVENTION: A method for ranking sequences to
; select target sequence zones of nucleic acids.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Daniel F. Perez
; STREET: 703 McKinney Ave., Suite 316
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Dos 6.0
; SOFTWARE: Wordperfect 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,507
; FILING DATE: 07-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perez, Daniel F.
; REGISTRATION NUMBER: 33,755
; REFERENCE/DOCKET NUMBER: 1110-2012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 871-1677
; TELEFAX: (214) 817-1083
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-320-507-11
;
; Query Match 100.0%; Score 20; DB 7; Length 24;
; Best Local Similarity 100.0%; Pred. No. 7.4e+02;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
|
Db 2 AGAGAGAGAGAGAGAGAG 21

RESULT 10

US-09-487-130-1/c
; Sequence 1, Application US/09487130
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: HASHEM, GIHAN M.
; TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED
; FILE REFERENCE: 91556/66385CIP
; CURRENT APPLICATION NUMBER: US/09/487,130
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 09/357,424
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid
US-09-487-130-1

Query Match 100.0%; Score 20; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
|
Db 24 AGAGAGAGAGAGAGAGAG 5

RESULT 11

US-09-487-130-2
; Sequence 2, Application US/09487130
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: HASHEM, GIHAN M.
; TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED
; FILE REFERENCE: 91556/66385CIP
; CURRENT APPLICATION NUMBER: US/09/487,130
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 09/357,424
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid
US-09-487-130-2

Query Match 100.0%; Score 20; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
|
Db 1 agagagagagagagagagag 20

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
|
Db 2 AGAGAGAGAGAGAGAGAG 21

RESULT 10

US-09-487-130-1/c
; Sequence 1, Application US/09487130
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: HASHEM, GIHAN M.
; TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED
; FILE REFERENCE: 91556/66385CIP
; CURRENT APPLICATION NUMBER: US/09/487,130
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 09/357,424
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid
US-09-487-130-1

Query Match 100.0%; Score 20; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
|
Db 24 AGAGAGAGAGAGAGAGAG 5

RESULT 11

US-09-487-130-2
; Sequence 2, Application US/09487130
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: HASHEM, GIHAN M.
; TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED
; FILE REFERENCE: 91556/66385CIP
; CURRENT APPLICATION NUMBER: US/09/487,130
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 09/357,424
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid
US-09-487-130-2

Query Match 100.0%; Score 20; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
|
Db 1 agagagagagagagagagag 20

RESULT 12

US-09-487-130-3/c
; Sequence 3, Application US/09487130
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: HASHEM, GIHAN M.
; TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED
; FILE REFERENCE: 91556/66385CIP
; CURRENT APPLICATION NUMBER: US/09/487,130
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 09/357,424
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid
US-09-487-130-3

Query Match 100.0%; Score 20; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
|
Db 24 AGAGAGAGAGAGAGAGAG 5

RESULT 13

US-09-487-130-4/c
; Sequence 4, Application US/09487130
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: HASHEM, GIHAN M.
; TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED
; FILE REFERENCE: 91556/66385CIP
; CURRENT APPLICATION NUMBER: US/09/487,130
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 09/357,424
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid
US-09-487-130-4

Query Match 100.0%; Score 20; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
|
Db 24 AGAGAGAGAGAGAGAGAG 5

RESULT 14

US-09-487-130-5
; Sequence 5, Application US/09487130

; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: HASHEM, GIHAN M.
; TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED
; TITLE OF INVENTION: DUPLEX
; FILE REFERENCE: 91556/66385CIP
; CURRENT APPLICATION NUMBER: US/09/487,130
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 09/357,424
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid
US-09-487-130-5

Query Match 100.0%; Score 20; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||
Db 1 agagagagagagagagag 20

RESULT 15
US-09-487-130-6/c
; Sequence 6, Application US/09487130
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: HASHEM, GIHAN M.
; TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED
; TITLE OF INVENTION: DUPLEX
; FILE REFERENCE: 91556/66385CIP
; CURRENT APPLICATION NUMBER: US/09/487,130
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 09/357,424
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid
US-09-487-130-6

Query Match 100.0%; Score 20; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||
Db 24 AGAGAGAGAGAGAGAGAG 5

Search completed: August 25, 2002, 00:32:25
Job time: 16383 sec

; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 908
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-908

Query Match 100.0%; Score 20; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
Db 22 AGAGAGAGAGAGAGAGAG 3

RESULT 3
US-10-112-653-877/c
; Sequence 877, Application US/10112653
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 877
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-877

Query Match 100.0%; Score 20; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
Db 22 AGAGAGAGAGAGAGAGAG 3

RESULT 4
US-10-078-757B-36
; Sequence 36, Application US/10078757B
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F., III
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0 Conl
; CURRENT APPLICATION NUMBER: US/10/078,757B
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 08/986,016
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36

; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PCR Primer
US-10-078-757B-36

Query Match 100.0%; Score 20; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
Db 1 agagagagagagagagagag 20

RESULT 5
US-10-205-303-285/c
; Sequence 265, Application US/10205303
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P120C2
; CURRENT APPLICATION NUMBER: US/10/205,303
; CURRENT FILING DATE: 2002-07-26
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 3506
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 265
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-303-285

Query Match 100.0%; Score 20; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
Db 44 AGAGAGAGAGAGAGAGAG 25

RESULT 6
US-10-027-632-20865/c
; Sequence 20865, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20865
; LENGTH: 95

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-20865

Query Match 100.0%; Score 20; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
Db 61 AGAGAGAGAGAGAGAGAG 42
|||||

RESULT 7

US-10-105-299-8877/c
; Sequence 8877, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8877
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-8877

Query Match 100.0%; Score 20; DB 7; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
Db 54 AGAGAGAGAGAGAGAGAG 35
|||||

RESULT 8

US-09-620-393B-3516
; Sequence 3516, Application US/09620393B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1068P
; CURRENT APPLICATION NUMBER: US/09/620,393B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9948
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3516
; LENGTH: 107
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..107
; OTHER INFORMATION: any n = a, g, c, t, unknown, or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..107
; OTHER INFORMATION: Ceres Seq. ID 1385553
US-09-620-393B-3516

Query Match 100.0%; Score 20; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
Db 62 agagagagagagagagagag 81
|||||

RESULT 9

US-60-319-414-2115
; Sequence 2115, Application US/60319414
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE NUCLEIC ACID
; FILE REFERENCE: P-FC-8-C1
; CURRENT APPLICATION NUMBER: US/60/319,414
; CURRENT FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 2313
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2115
; LENGTH: 111
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (81)..(81)
; OTHER INFORMATION: n = unknown
US-60-319-414-2115

Query Match 100.0%; Score 20; DB 8; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
Db 2 agagagagagagagagagag 21
|||||

RESULT 10

US-09-620-393B-6947
; Sequence 6947, Application US/09620393B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1068P
; CURRENT APPLICATION NUMBER: US/09/620,393B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9948
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6947
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..117
; OTHER INFORMATION: any n = a, g, c, t, unknown, or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..117
; OTHER INFORMATION: Ceres Seq. ID 1395310
US-09-620-393B-6947

Query Match 100.0%; Score 20; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
|||||

Db 56 agagagagagagagagagag 75

RESULT 11
US-09-620-393B-7088
; Sequence 7088, Application US/09620393B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1068P
; CURRENT APPLICATION NUMBER: US/09/620.393B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9948
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7088
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..123
; OTHER INFORMATION: any n = a, g, c, t, unknown, or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..123
; OTHER INFORMATION: Ceres Seq. ID I396411
US-09-620-393B-7088

Query Match 100.0%; Score 20; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||

Db 85 agagagagagagagagag 104
|||||

RESULT 12
US-10-057-940-12
; Sequence 12, Application US/10057940
; GENERAL INFORMATION:
; APPLICANT: Pantoliano, Michael W.
; APPLICANT: Salemm, F. Raymond
; TITLE OF INVENTION: High Throughput Method for Functionally Classifying Proteins
; FILE OF INVENTION: Identified Using a Genomics Approach
; FILE REFERENCE: 1503.0310002/JAG/JSO
; CURRENT APPLICATION NUMBER: US/10/057,940
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/190,128
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/065,129
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CT- and GA-rich tract
US-10-057-940-12

Query Match 100.0%; Score 20; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||

Db 66 agagagagagagagagagag 85
|||||

RESULT 13
US-10-057-940-12/c
; Sequence 12, Application US/10057940
; GENERAL INFORMATION:
; APPLICANT: Pantoliano, Michael W.
; APPLICANT: Salemm, F. Raymond
; APPLICANT: Carver, Jr., Theodore, E.
; TITLE OF INVENTION: High Throughput Method for Functionally Classifying Proteins
; FILE OF INVENTION: Identified Using a Genomics Approach
; FILE REFERENCE: 1503.0310002/JAG/JSO
; CURRENT APPLICATION NUMBER: US/10/057,940
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/190,128
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/065,129
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CT- and GA-rich tract
US-10-057-940-12

Query Match 100.0%; Score 20; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||

Db 64 AGAGAGAGAGAGAGAGAG 45
|||||

RESULT 14
US-10-057-940-13
; Sequence 13, Application US/10057940
; GENERAL INFORMATION:
; APPLICANT: Pantoliano, Michael W.
; APPLICANT: Salemm, F. Raymond
; APPLICANT: Carver, Jr., Theodore, E.
; TITLE OF INVENTION: High Throughput Method for Functionally Classifying Proteins
; FILE OF INVENTION: Identified Using a Genomics Approach
; FILE REFERENCE: 1503.0310002/JAG/JSO
; CURRENT APPLICATION NUMBER: US/10/057,940
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/190,128
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/065,129
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AG- and TC-rich tract
US-10-057-940-13

Query Match 100.0%; Score 20; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||

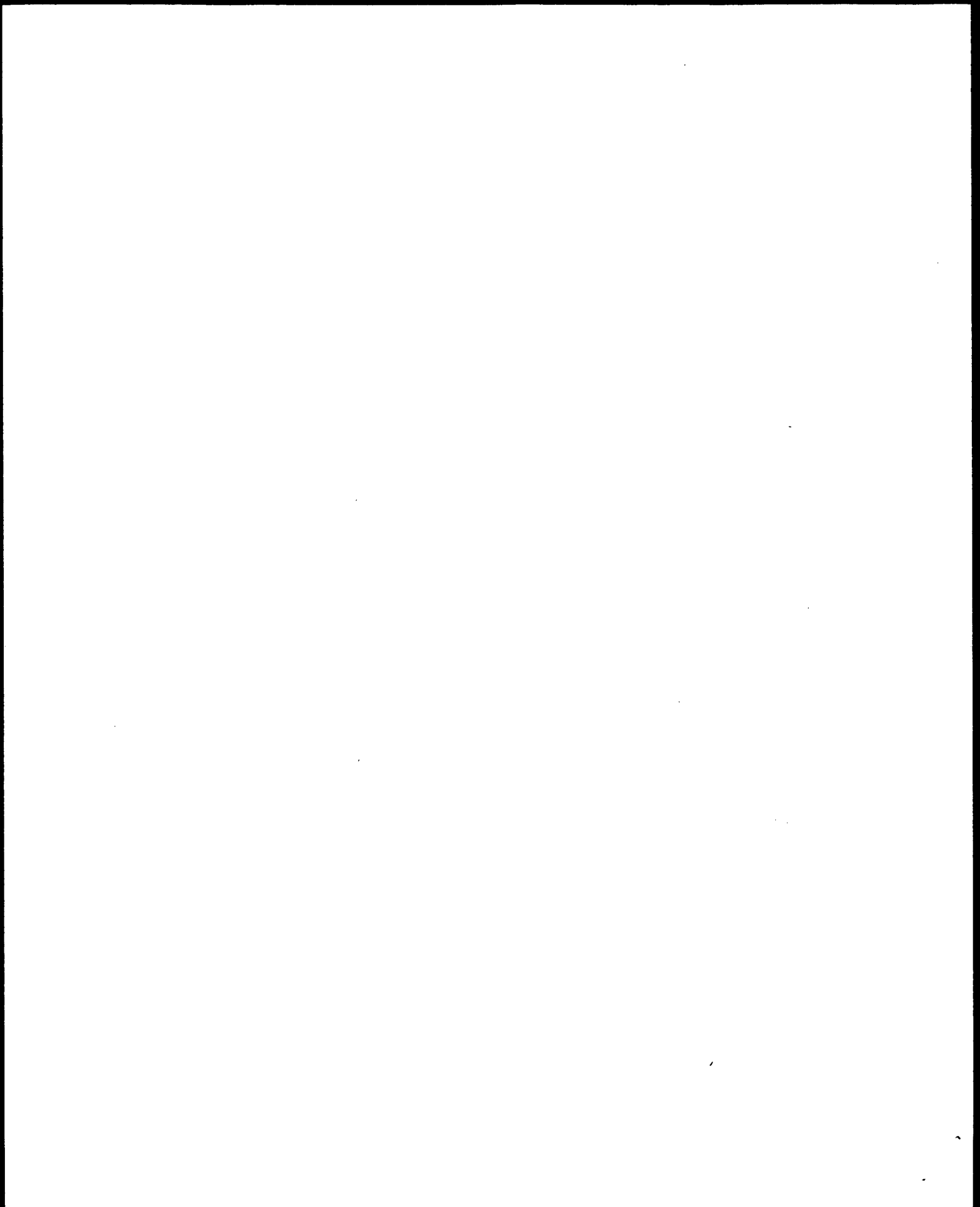
Db 1 agagagagagagagagagag 20
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RESULT 15
US-10-057-940-13/c
; Sequence 13, Application US/10057940
; GENERAL INFORMATION:
; APPLICANT: Pantoliano, Michael W.
; APPLICANT: Salenme, F. Raymond
; APPLICANT: Carver, Jr., Theodore, E.
; TITLE OF INVENTION: High Throughput Method for Functionally Classifying Proteins
; TITLE OF INVENTION: Identified Using a Genomics Approach
; FILE REFERENCE: 1503.0310002/JAG/JSO
; CURRENT APPLICATION NUMBER: US/10/057,940
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/190,128
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/065,129
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AG- and TC-rich tract
US-10-057-940-13

Query Match 100.0%; Score 20; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 20
|||||
Db 127 AGAGAGAGAGAGAGAG 108

Search completed: August 25, 2002, 00:45:46
Job time: 12373 sec



c 32 0 0.0 1 24 US-09-625-102-614 Sequence 614, App
 c 33 0 0.0 1 24 US-09-625-102-836 Sequence 836, App
 c 34 0 0.0 1 24 US-09-625-102-836 Sequence 836, App
 c 35 0 0.0 1 24 US-09-625-102-895 Sequence 895, App
 c 36 0 0.0 1 24 US-09-625-102-895 Sequence 895, App
 c 37 0 0.0 1 24 US-09-625-102-982 Sequence 982, App
 c 38 0 0.0 1 24 US-09-625-102-982 Sequence 982, App
 c 39 0 0.0 1 24 US-09-625-102-1048 Sequence 1048, App
 c 40 0 0.0 1 24 US-09-625-102-1048 Sequence 1048, App
 c 41 0 0.0 1 24 US-09-625-102-1352 Sequence 1352, App
 c 42 0 0.0 1 24 US-09-625-102-1352 Sequence 1352, App
 c 43 0 0.0 1 24 US-09-634-306B-51773 Sequence 51773, A
 c 44 0 0.0 1 24 US-09-634-306B-51773 Sequence 51773, A
 c 45 0 0.0 1 24 US-09-634-306B-51841 Sequence 51841, A

ALIGNMENTS

RESULT 1
 PCT-US93-00977-702
 ; Sequence 702, Application PC/TUS9300977
 ; GENERAL INFORMATION:

; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA

; NUMBER OF SEQUENCES: 711

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson, and Bear

; STREET: 620 Newport Center Dr. Sixteenth Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: USA

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/00977

; FILING DATE: 19930129

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E.

; REGISTRATION NUMBER: 34,115

; REFERENCE/DOCKET NUMBER: HITACHI.006H

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 714-760-0404

; TELEFAX: 714-760-9502

; INFORMATION FOR SEQ ID NO: 702:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

PCT-US93-00977-702

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 A 1

RESULT 2

PCT-US93-00977-702/c

; Sequence 702, Application PC/TUS9300977

; GENERAL INFORMATION:

; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA

; NUMBER OF SEQUENCES: 711

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson, and Bear

; STREET: 620 Newport Center Dr. Sixteenth Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: USA

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/00977

; FILING DATE: 19930129

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E.

; REGISTRATION NUMBER: 34,115

; REFERENCE/DOCKET NUMBER: HITACHI.006H

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 714-760-0404

; TELEFAX: 714-760-9502

; INFORMATION FOR SEQ ID NO: 702:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

PCT-US93-00977-702

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 T 1

RESULT 3

US-08-068-298-17

; Sequence 17, Application US/08068298

; GENERAL INFORMATION:

; APPLICANT: MUENCHAU, DARYL, ET AL.

; TITLE OF INVENTION: METHOD FOR GENERATING APTAMERS OF

; TITLE OF INVENTION: NON-PREDETERMINED OR SUBSTANTIALLY

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LYON & LYON

; STREET: 611 West Sixth St.

; CITY: Los Angeles

; STATE: CA

; COUNTRY: USA

; ZIP: 90017

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/068,298

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/659,980

; FILING DATE: February 21, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CONSALVI, MARY S
; REGISTRATION NUMBER: 32,212
; REFERENCE/DOCKET NUMBER: 193/051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; FEATURE:
; OTHER INFORMATION: where N also may be isoguanine or
; OTHER INFORMATION: isocytostine
; US-08-068-298-17

Query Match 0.0%; Score 0; DB 4; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 G 1

RESULT 4

; Sequence 17, Application US/08068298
; GENERAL INFORMATION:
; APPLICANT: MUENCHAU, DARYL, ET AL.
; TITLE OF INVENTION: METHOD FOR GENERATING APTAMERS OF
; TITLE OF INVENTION: NON-PREDETERMINED OR SUBSTANTIALLY
; TITLE OF INVENTION: NON-PREDETERMINED SEQUENCES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 611 West Sixth St.
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,298
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/659,980
; FILING DATE: February 21, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CONSALVI, MARY S
; REGISTRATION NUMBER: 32,212
; REFERENCE/DOCKET NUMBER: 193/051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; FEATURE:

; OTHER INFORMATION: where N also may be isoguanine or
; OTHER INFORMATION: isocytostine
; US-08-068-298-17

Query Match 0.0%; Score 0; DB 4; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 C 1

RESULT 5

; Sequence 9, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.
; APPLICANT: Reenan, Robert A.G.
; APPLICANT: Fishel, Richard
; TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 A 1

RESULT 6

; Sequence 9, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.

```

; APPLICANT: Reenan, Robert A.G.
; APPLICANT: Fishel, Richard
; TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 T 1

RESULT 7
US-08-154-792A-24
; Sequence 24, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.
; APPLICANT: Reenan, Robert A.G.
; APPLICANT: Fishel, Richard
; TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-24

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; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-24

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 A 1

RESULT 8
US-08-154-792A-24/c
; Sequence 24, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.
; APPLICANT: Reenan, Robert A.G.
; APPLICANT: Fishel, Richard
; TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-24

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Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
 Db 1 T 1

RESULT 9
 US-08-163-449A-9
 ; Sequence 9, Application US/08163449A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kolodner, Richard D.
 ; APPLICANT: Reenan, Robert A.G.
 ; APPLICANT: Fishel, Richard
 ; TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 ; TITLE OF INVENTION: PRODUCTS,
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 ; ADDRESSEE: ROBERTS & CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/163.449A
 ; FILING DATE: 07-DEC-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Resnick, David S.
 ; REGISTRATION NUMBER: 34,234
 ; REFERENCE/DOCKET NUMBER: 44824-CIP-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 523-3400
 ; TELEFAX: (617) 523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-163-449A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
 Db 1 A 1

RESULT 10
 US-08-163-449A-9/c
 ; Sequence 9, Application US/08163449A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kolodner, Richard D.
 ; APPLICANT: Reenan, Robert A.G.
 ; APPLICANT: Fishel, Richard

; TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 ; TITLE OF INVENTION: PRODUCTS,
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 ; ADDRESSEE: ROBERTS & CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/163.449A
 ; FILING DATE: 07-DEC-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Resnick, David S.
 ; REGISTRATION NUMBER: 34,234
 ; REFERENCE/DOCKET NUMBER: 44824-CIP-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 523-3400
 ; TELEFAX: (617) 523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-163-449A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
 Db 1 T 1

RESULT 11
 US-08-163-449A-24
 ; Sequence 24, Application US/08163449A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kolodner, Richard D.
 ; APPLICANT: Reenan, Robert A.G.
 ; APPLICANT: Fishel, Richard
 ; TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 ; TITLE OF INVENTION: PRODUCTS,
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 ; ADDRESSEE: ROBERTS & CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/163,449A
FILING DATE: 07-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,234
REFERENCE/DOCKET NUMBER: 44824-CIP-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-163-449A-24

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 n 1
DB 1 A 1

RESULT 12
US-08-163-449A-24/c
Sequence 24, Application US/08163449A
GENERAL INFORMATION:
APPLICANT: Kolodner, Richard D.
APPLICANT: Reenan, Robert A.G.
APPLICANT: Fishel, Richard
TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
TITLE OF INVENTION: PRODUCTS,
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
ADDRESSEE: ROBERTS & CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/163,449A
FILING DATE: 07-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,234
REFERENCE/DOCKET NUMBER: 44824-CIP-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-163-449A-24

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 n 1
DB 1 T 1

RESULT 13
US-08-208-572-10
Sequence 10, Application US/08208572
GENERAL INFORMATION:
APPLICANT: Silberstein Ph.D., David S.
APPLICANT: Balczewicz-Sablinska M.D., Maria K.
APPLICANT: Newman Ph.D., Gale W.
TITLE OF INVENTION: CONTROL OF HIV GROWTH WITH ECEF AND
TITLE OF INVENTION: ECEF
TITLE OF INVENTION: DERIVATIVES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL, & STEWART
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,572
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan Esq., Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: 092662-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5020
TELEFAX: (617) 227-7566
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-208-572-10

Query Match 0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 n 1
DB 1 A 1

RESULT 14
US-08-208-572-10/c
Sequence 10, Application US/08208572
GENERAL INFORMATION:
APPLICANT: Silberstein Ph.D., David S.
APPLICANT: Balczewicz-Sablinska M.D., Maria K.
APPLICANT: Newman Ph.D., Gale W.
TITLE OF INVENTION: CONTROL OF HIV GROWTH WITH ECEF AND


```

; TITLE OF INVENTION: ECEF
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL, & STEWART
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,572
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan Esq., Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: 092662-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-5020
; TELEFAX: (617) 227-7566
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-208-572-10

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Query Match          0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

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QY      1 n 1
Db      1 T 1

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RESULT 15
US-08-237-491-6868
; Sequence 6868, Application US/08237491
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey
; APPLICANT: Delegeane, Angelo
; APPLICANT: Jernigan, Colleen
; APPLICANT: Levine, Wendy B.
; TITLE OF INVENTION: SHEAR-STRESSED HUMAN UMBILICAL VEIN
; ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 7326
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,491
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/137,951
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,801
; FILING DATE: 17-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8135-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: Z-068903
; US-08-237-491-6868

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Query Match          0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

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```

QY      1 n 1
Db      1 C 1

```

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Search completed: August 25, 2002, 00:32:25
Job time: 16383 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 00:45:46 ; Search time 787.61 Seconds
(without alignments)
69.294 Million cell updates/sec

Title: US-10-077-383-30
Perfect score: 20
Sequence: 1 nnnnnnnnnnnnnnnnnnn 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1737567 seqs, 1364410299 residues

Total number of hits satisfying chosen parameters: 3475134

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Pending Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/JS06_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/JS07_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/JS08_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/JS09_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/JS10_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/JS10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/JS10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/JS60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	0	0.0	1	7	US-10-027-632-51773
2	0	0.0	1	7	US-10-027-632-51773
3	0	0.0	1	7	US-10-027-632-51841
4	0	0.0	1	7	US-10-027-632-51841
5	0	0.0	1	7	US-10-027-632-52001
6	0	0.0	1	7	US-10-027-632-52051
7	0	0.0	1	7	US-10-027-632-52051
8	0	0.0	1	7	US-10-027-632-52051
9	0	0.0	1	7	US-10-027-632-52156
10	0	0.0	1	7	US-10-027-632-52156
11	0	0.0	1	7	US-10-027-632-52157
12	0	0.0	1	7	US-10-027-632-52157
13	0	0.0	1	7	US-10-027-632-52177
14	0	0.0	1	7	US-10-027-632-52177
15	0	0.0	1	7	US-10-027-632-52215
16	0	0.0	1	7	US-10-027-632-52215
17	0	0.0	1	7	US-10-027-632-52240
18	0	0.0	1	7	US-10-027-632-52240
19	0	0.0	1	7	US-10-027-632-52272
20	0	0.0	1	7	US-10-027-632-52272
21	0	0.0	1	7	US-10-027-632-52624
22	0	0.0	1	7	US-10-027-632-52624
23	0	0.0	1	7	US-10-027-632-52642
24	0	0.0	1	7	US-10-027-632-52642
25	0	0.0	1	7	US-10-027-632-52668

c	26	0	0.0	1	7	US-10-027-632-52668	Sequence 52668, A
c	27	0	0.0	1	7	US-10-027-632-52677	Sequence 52677, A
c	28	0	0.0	1	7	US-10-027-632-52677	Sequence 52677, A
c	29	0	0.0	1	7	US-10-027-632-52707	Sequence 52707, A
c	30	0	0.0	1	7	US-10-027-632-52707	Sequence 52707, A
c	31	0	0.0	1	7	US-10-027-632-52714	Sequence 52714, A
c	32	0	0.0	1	7	US-10-027-632-52714	Sequence 52714, A
c	33	0	0.0	1	7	US-10-027-632-52721	Sequence 52721, A
c	34	0	0.0	1	7	US-10-027-632-52721	Sequence 52721, A
c	35	0	0.0	1	7	US-10-027-632-52776	Sequence 52776, A
c	36	0	0.0	1	7	US-10-027-632-52776	Sequence 52776, A
c	37	0	0.0	1	7	US-10-027-632-52863	Sequence 52863, A
c	38	0	0.0	1	7	US-10-027-632-52863	Sequence 52863, A
c	39	0	0.0	1	7	US-10-027-632-52864	Sequence 52864, A
c	40	0	0.0	1	7	US-10-027-632-52864	Sequence 52864, A
c	41	0	0.0	1	7	US-10-027-632-52891	Sequence 52891, A
c	42	0	0.0	1	7	US-10-027-632-52891	Sequence 52891, A
c	43	0	0.0	1	7	US-10-027-632-58290	Sequence 58290, A
c	44	0	0.0	1	7	US-10-027-632-58290	Sequence 58290, A
c	45	0	0.0	1	7	US-10-027-632-58459	Sequence 58459, A

ALIGNMENTS

RESULT 1
US-10-027-632-51773
; Sequence 51773, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51773
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51773

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

RESULT 2
US-10-027-632-51773/c
; Sequence 51773, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

;; TITLE OF INVENTION: Polymorphisms in the Human Genome
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-08-09
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 51773
;; LENGTH: 1
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-51773

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 G 1

RESULT 3
US-10-027-632-51841
;; Sequence 51841, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 51841
;; LENGTH: 1
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-51841

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 y 1
RESULT 4
US-10-027-632-51841/C
;; Sequence 51841, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 51841
;; LENGTH: 1
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-51841

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 R 1

RESULT 5
US-10-027-632-52001
;; Sequence 52001, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52001
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52001

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 y 1

RESULT 6

US-10-027-632-52001/c
; Sequence 52001, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52001
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52001

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 r 1

RESULT 7

US-10-027-632-52051
; Sequence 52051, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52051
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52051

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

RESULT 8

US-10-027-632-52051/c
; Sequence 52051, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52051
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52051

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 g 1

RESULT 9

US-10-027-632-52156
; Sequence 52156, Application US/10027632
; GENERAL INFORMATION:

```

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52156
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52156

```

```

Query Match          0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 n 1
Db 1 c 1

```

```

RESULT 10
US-10-027-632-52156/c
; Sequence 52156, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52156
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52156

```

```

Query Match          0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;

```

```

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 n 1
Db 1 G 1

```

```

RESULT 11
US-10-027-632-52157
; Sequence 52157, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52157
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52157

```

```

Query Match          0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 n 1
Db 1 c 1

```

```

RESULT 12
US-10-027-632-52157/c
; Sequence 52157, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09

```

; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 52157
 ; LENGTH: 1
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-52157

Query Match 0.0%; Score 0; DB 7; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 G 1

RESULT 13
 US-10-027-632-52177
 ; Sequence 52177, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027.632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 52177
 ; LENGTH: 1
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-52177

Query Match 0.0%; Score 0; DB 7; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 c 1

RESULT 14
 US-10-027-632-52177/c
 ; Sequence 52177, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027.632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 52177
 ; LENGTH: 1
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-52177

Query Match 0.0%; Score 0; DB 7; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 G 1

RESULT 15
 US-10-027-632-52215
 ; Sequence 52215, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027.632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 52215
 ; LENGTH: 1
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-52215

Query Match 0.0%; Score 0; DB 7; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 c 1

Search completed: August 25, 2002, 00:45:46

Mon Aug 26 10:18:10 2002

us-10-077-383-30.rnpn

Page 6

Job time: 12373 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 00:32:25 ; Search time 8635 Seconds
(without alignments)
45.099 Million cell updates/sec

Title: US-10-077-383-31

Perfect score: 18

Sequence: 1 agagagagagagagag 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues 43959072

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

- 1: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US08_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
- 8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*
- 9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
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- 21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
- 22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
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- 26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
- 27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
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- 29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
- 30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*
- 31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
- 32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
- 33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*
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- 35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
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- 37: /cgn2_6/ptodata/2/pna/US100_COMB.seq:*
- 38: /cgn2_6/ptodata/2/pna/US101_COMB.seq:*
- 39: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
- 40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
- 41: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
- 42: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
- 43: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*

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66: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*

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74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*

75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	18	100.0	18	7	US-08-309-335A-515
2	18	100.0	18	9	US-08-531-241A-515
3	18	100.0	18	16	US-09-263-959-515
4	18	100.0	20	14	US-09-081-385-40
5	18	100.0	20	22	US-09-589-606-40
6	18	100.0	20	28	US-09-700-354A-40
7	18	100.0	20	29	US-09-752-639-40
8	18	100.0	20	36	US-09-984-198-40
9	18	100.0	21	7	US-08-309-335A-807
10	18	100.0	21	9	US-08-531-241A-807
11	18	100.0	21	16	US-09-263-959-807
12	18	100.0	21	24	US-09-634-320-5
13	18	100.0	21	24	US-09-634-320-10
14	18	100.0	22	24	US-09-634-320-6
15	18	100.0	22	26	US-09-669-187A-908
16	18	100.0	22	37	US-10-017-995-908
17	18	100.0	24	7	US-08-320-507-8
18	18	100.0	24	7	US-08-320-507-9
19	18	100.0	24	7	US-08-320-507-10
20	18	100.0	24	7	US-08-320-507-11
21	18	100.0	24	18	US-09-487-130-1
22	18	100.0	24	18	US-09-487-130-2
23	18	100.0	24	18	US-09-487-130-3
24	18	100.0	24	18	US-09-487-130-4
25	18	100.0	24	18	US-09-487-130-5
26	18	100.0	24	18	US-09-487-130-6
27	18	100.0	25	35	US-09-956-584-462936
28	18	100.0	25	35	US-09-956-584-470373
29	18	100.0	25	35	US-09-956-584-470381
30	18	100.0	25	35	US-09-956-584-570427
31	18	100.0	25	35	US-09-956-584-570432

Sequence 515, App
Sequence 515, App
Sequence 515, App
Sequence 40, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 807, App
Sequence 807, App
Sequence 5, Appl
Sequence 10, Appl
Sequence 6, Appl
Sequence 908, App
Sequence 908, App
Sequence 8, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 462936,
Sequence 470373,
Sequence 470381,
Sequence 570427,
Sequence 570432,

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.425C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 515:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-515

Query Match 100.0%; Score 13; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
| | | | | | | | | | | | | | | | | | | |
Db 1 AGAGAGAGAGAGAGAGAG 18

RESULT 4

US-09-081-385-40/c
Sequence 40, Application US/09081385
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081.385
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/081.385
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 08/964.747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030.761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-081-385-40

Query Match 100.0%; Score 18; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 agagagagagagagagag 18
| | | | | | | | | | | | | | | | | | | |
Db 19 AGAGAGAGAGAGAGAGAG 2

RESULT 5

US-09-589-606-40/c
Sequence 40, Application US/09589606
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589.606
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 09/081.385
FILING DATE:
APPLICATION NUMBER: 08/964.747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030.761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-589-606-40

Query Match 100.0%; Score 18; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
| | | | | | | | | | | | | | | | | | | |
Db 19 AGAGAGAGAGAGAGAGAG 2

RESULT 6

US-09-700-354A-40/c
Sequence 40, Application US/09700354A
GENERAL INFORMATION:
APPLICANT: Gatanaga, Tetsuya

```

; Granger, Gale A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BOZICEVIC, FIELD, & FRANCIS, LLP
; STREET: 200 MIDDLEFIELD ROAD, #200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/700,354A
; FILING DATE: 17-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/081,385
; FILING DATE: 14-MAY-1998
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE: 14-MAY-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Francis, Carol L.
; REGISTRATION NUMBER: 36,513
; REFERENCE/DOCKET NUMBER: IRVN-007CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-700-354A-40

Query Match 100.0%; Score 18; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
Db 19 AGAGAGAGAGAGAGAG 2

RESULT 7
US-09-752-639-40/c
; Sequence 40, Application US/09752639
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,198
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997

```

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; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,639
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-752-639-40

```

```

Query Match 100.0%; Score 18; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
Db 19 AGAGAGAGAGAGAGAG 2

```

```

RESULT 8
US-09-984-198-40/c
; Sequence 40, Application US/09984198
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,198
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997

```

APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-984-198-40

Query Match 100.0%; Score 18; DB 36; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
Db 19 AGAGAGAGAGAGAGAG 2

RESULT 9

US-08-309-335A-807/c
Sequence 807, Application US/08309335A
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,335A
FILING DATE: 19-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 807:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-309-335A-807

Query Match 100.0%; Score 13; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
Db 21 AGAGAGAGAGAGAGAG 4

RESULT 10

US-08-531-241A-807/c
Sequence 807, Application US/08531241A
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,241A
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 807:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-531-241A-807

Query Match 100.0%; Score 18; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
Db 21 AGAGAGAGAGAGAGAG 4

RESULT 11

US-09-263-959-807/c
Sequence 807, Application US/09263959
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 807:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-807

```

```

Query Match      100.0%; Score 18; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 agagagagagagagagag 18
   |||||
Db 21 AGAGAGAGAGAGAGAG 4

```

```

RESULT 12
US-09-634-320-5/c
; Sequence 5, Application US/09634320
; GENERAL INFORMATION:
; APPLICANT: Papisov, Mikhail, I.
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
; FILE REFERENCE: 0838.1003-001
; CURRENT APPLICATION NUMBER: US/09/634,320
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/147,919
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-634-320-5

```

```

Query Match      100.0%; Score 18; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 agagagagagagagagag 18
   |||||
Db 21 AGAGAGAGAGAGAGAG 4

```

```

RESULT 13
US-09-634-320-10/c
; Sequence 10, Application US/09634320
; GENERAL INFORMATION:
; APPLICANT: Papisov, Mikhail, I.
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
; FILE REFERENCE: 0838.1003-001
; CURRENT APPLICATION NUMBER: US/09/634,320

```

```

; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/147,919
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-634-320-10

```

```

Query Match      100.0%; Score 18; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 agagagagagagagagag 18
   |||||
Db 21 AGAGAGAGAGAGAGAG 4

```

```

RESULT 14
US-09-634-320-6
; Sequence 6, Application US/09634320
; GENERAL INFORMATION:
; APPLICANT: Papisov, Mikhail, I.
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
; FILE REFERENCE: 0838.1003-001
; CURRENT APPLICATION NUMBER: US/09/634,320
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/147,919
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-634-320-6

```

```

Query Match      100.0%; Score 18; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 agagagagagagagagag 18
   |||||
Db 1 agagagagagagagagag 18

```

```

RESULT 15
US-09-669-187A-908/c
; Sequence 908, Application US/09669187A
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/669,187A
; CURRENT FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; NUMBER OF SEQ ID NOS: 1145

```

```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 908
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-669-187A-908
```

```
Query Match      100.0%; Score 18; DB 26; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 agagagagagagagagag 18
         |||||
Db       22 AGAGAGAGAGAGAGAG 5
```

```
Search completed: August 25, 2002, 00:32:16
Job time: 16384 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run On: August 25, 2002, 00:45:46 ; Search time 787.61 Seconds
(without alignments)
62.364 Million cell updates/sec

Title: US-10-077-383-31

Perfect score: 18

Sequence: 1 agagagagagagagagag 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1737567 seqs, 1364410299 residues

Total number of hits satisfying chosen parameters: 3475134

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	US-10-077-383-31
2	18	100.0	18	6	US-10-077-383-32
3	18	100.0	18	7	US-10-011-204-4
4	18	100.0	20	6	US-10-077-383-29
5	18	100.0	22	5	US-09-777-479-908
6	18	100.0	22	7	US-10-112-653-877
7	18	100.0	49	7	US-10-06C-848-11
8	18	100.0	50	5	US-09-997-672-29
9	18	100.0	50	5	US-09-196-447B-11
10	18	100.0	50	5	US-09-724-857-25
11	18	100.0	50	6	US-10-098-602A-7
12	18	100.0	50	7	US-10-105-624-36
13	18	100.0	50	7	US-10-082-894-7
14	18	100.0	50	7	US-10-16C-362-14
15	18	100.0	50	7	US-10-07E-757B-36
16	18	100.0	69	6	US-10-205-303-265
17	18	100.0	95	7	US-10-027-632-20865
18	18	100.0	102	7	US-10-105-299-8877
19	18	100.0	107	5	US-09-62C-393B-3516
20	18	100.0	111	8	US-60-315-414-2115
21	18	100.0	117	5	US-09-62C-393B-6947
22	18	100.0	123	5	US-09-62C-393B-7088
23	18	100.0	128	7	US-10-057-940-12
24	18	100.0	128	7	US-10-057-940-12
25	18	100.0	128	7	US-10-057-940-13

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c 26 18 100.0 128 7 US-10-057-940-13 Sequence 13, Appl
c 27 18 100.0 133 7 US-10-027-632-17565 Sequence 75765, A
c 28 18 100.0 140 7 US-10-027-632-178517 Sequence 178517,
c 29 18 100.0 140 7 US-10-027-632-178525 Sequence 178525,
c 30 18 100.0 140 7 US-10-027-632-178533 Sequence 178533,
c 31 18 100.0 146 5 US-09-804-068A-211 Sequence 211, App
c 32 18 100.0 150 7 US-10-027-632-177965 Sequence 177965,
c 33 18 100.0 152 6 US-10-035-832-323 Sequence 323, App
c 34 18 100.0 162 5 US-09-171-209-17 Sequence 17, Appl
c 35 18 100.0 162 8 US-60-377-240-4986 Sequence 4986, Ap
c 36 18 100.0 163 5 US-09-539-331D-40551 Sequence 40551, A
c 37 18 100.0 166 5 US-09-539-331D-39401 Sequence 39401, A
c 38 18 100.0 166 5 US-09-171-209-16 Sequence 16, Appl
c 39 18 100.0 173 5 US-09-539-331D-40097 Sequence 40097, A
c 40 18 100.0 174 5 US-09-886-492-7415 Sequence 7415, Ap
c 41 18 100.0 176 5 US-09-539-800C-7050 Sequence 7050, Ap
c 42 18 100.0 179 5 US-09-963-137-115 Sequence 115, App
c 43 18 100.0 183 5 US-09-539-331D-12512 Sequence 12512, A
c 44 18 100.0 185 8 US-60-382-445-235 Sequence 235, App
c 45 18 100.0 187 5 US-09-539-331D-40315 Sequence 40315, A

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ALIGNMENTS

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RESULT 1
US-10-077-383-31
; Sequence 31, Application US/10077383
; GENERAL INFORMATION:
; APPLICANT: Haydock, Paul V.
; APPLICANT: U'Ren, Jack
; APPLICANT: Saigene Corporation
; TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and
; FILE OF INVENTION: DNA/RNA Mixed Polymer Intermediate Products
; FILE REFERENCE: 018048-001710US
; CURRENT APPLICATION NUMBER: US/10/077,383
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/296,812
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:(XY)-n spacer
; OTHER INFORMATION: sequence, where X = a, Y = g and n = 9
US-10-077-383-31

```

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Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 agagagagagagagagag 18
Db 1 agagagagagagagagag 18

```

```

RESULT 2
US-10-077-383-32/c
; Sequence 32, Application US/10077383
; GENERAL INFORMATION:
; APPLICANT: Haydock, Paul V.
; APPLICANT: U'Ren, Jack
; APPLICANT: Saigene Corporation
; TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and
; FILE OF INVENTION: DNA/RNA Mixed Polymer Intermediate Products
; FILE REFERENCE: 018048-001710US
; CURRENT APPLICATION NUMBER: US/10/077,383
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/296,812

```

; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:(XY)-n spacer
; OTHER INFORMATION: sequence complement, where X = a, Y = g and n = 9
US-10-077-383-32

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
|||||

Db 18 AGAGAGAGAGAGAGAG 1

RESULT 3

US-10-011-204-4/c
; Sequence 4, Application US/10011204
; GENERAL INFORMATION:
; APPLICANT: EKINS, Roger P
; TITLE OF INVENTION: Binding assay using binding agents with tail groups
; FILE REFERENCE: 0380-P01180US0
; CURRENT APPLICATION NUMBER: US/10/011,204
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US/08/700,530
; PRIOR FILING DATE: 1996-10-23
; PRIOR APPLICATION NUMBER: PCT/GB95/00521
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: GB 9404709.9
; PRIOR FILING DATE: 1994-03-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-011-204-4

Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
|||||

Db 18 AGAGAGAGAGAGAGAG 1

RESULT 4

US-10-077-383-29
; Sequence 29, Application US/10077393
; GENERAL INFORMATION:
; APPLICANT: Haydock, Paul V.
; APPLICANT: U'Ren, Jack
; APPLICANT: Saigene Corporation
; TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and
; FILE REFERENCE: 018048-001710US
; CURRENT APPLICATION NUMBER: US/10/077,383
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/296,812
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:(XY)-n spacer
; OTHER INFORMATION: sequence, where X = a and Y = g
; NAME/KEY: modified_base
; LOCATION: (13)..(20)
; OTHER INFORMATION: a or g at positions 13-20 may be present or absent
US-10-077-383-29

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
|||||

Db 1 agagagagagagagagag 18

RESULT 5

US-09-776-479-908/c
; Sequence 908, Application US/09776479
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 908
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-908

Query Match 100.0%; Score 18; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
|||||

Db 22 AGAGAGAGAGAGAGAG 5

RESULT 6

US-10-112-653-877/c
; Sequence 877, Application US/10112653
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 877
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-877

Query Match 100.0%; Score 18; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
| | | | | | | | | | | | | | | | | |
Db 22 AGAGAGAGAGAGAGAG 5

RESULT 7
US-10-060-848-11
; Sequence 11, Application US/10060848
; GENERAL INFORMATION:
; APPLICANT: Kloeck, Andrew
; APPLICANT: Williams, Deryck Jeremy
; APPLICANT: Salmon, Brandy Leigh
; TITLE OF INVENTION: NEMATODE MDH-LIKE SEQUENCE
; FILE REFERENCE: 12557-002001
; CURRENT APPLICATION NUMBER: US/10/060,848
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/266,037
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Universal primer to poly A tail
US-10-060-848-11

Query Match 100.0%; Score 18; DB 7; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
| | | | | | | | | | | | | | | | | |
Db 2 agagagagagagagagag 19

RESULT 8
US-09-997-672-29
; Sequence 29, Application US/09997672
; GENERAL INFORMATION:
; APPLICANT: Weterings, Koen
; APPLICANT: Apuya, Nestor R.
; APPLICANT: Tatarinova, Tatiana
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; APPLICANT: Ceres, Inc.
; TITLE OF INVENTION: Polynucleotides Useful for Modulating Transcription
; FILE REFERENCE: 023070-115810US
; CURRENT APPLICATION NUMBER: US/09/997,672
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,672
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
; OTHER INFORMATION: linker-primer
US-09-997-672-29

Query Match 100.0%; Score 18; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
| | | | | | | | | | | | | | | | | |
Db 2 agagagagagagagagag 19

RESULT 9
US-09-196-447B-11
; Sequence 11, Application US/09196447B
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Grieve, Robert B.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,447B
; FILING DATE: 19-Nov-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-13-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..50
; OTHER INFORMATION: /label= PRIMER
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-196-447B-11

Query Match 100.0%; Score 18; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
| | | | | | | | | | | | | | | | | |
Db 2 AGAGAGAGAGAGAGAGAG 19

RESULT 10

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US-09-724-857-25
; Sequence 25, Application US/09724857
; GENERAL INFORMATION:
; APPLICANT: Weterings, Koen
; APPLICANT: Apaya, Nestor R.
; APPLICANT: Tatarinova, Tatiana
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: The Regents of the University of California
; FILE OF INVENTION: Polynucleotides Useful for Modulating Transcription
; CURRENT APPLICATION NUMBER: US/09724,857
; CURRENT FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
; OTHER INFORMATION: linker-primer
US-09-724-857-25

```

```

Query Match      100.0%; Score 18; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 agagagagagagagagag 18
Db 2 agagagagagagagagag 19

```

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RESULT 11
US-10-098-602A-7
; Sequence 7, Application US/10098602A
; GENERAL INFORMATION:
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Williams, Deryck Jeremy
; APPLICANT: Salmon, Brandy
; TITLE OF INVENTION: NEMATOIDE GS-LIKE SEQUENCES
; FILE REFERENCE: 12557-004001
; CURRENT APPLICATION NUMBER: US/10/098,602A
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/276,621
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-098-602A-7

```

```

Query Match      100.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 agagagagagagagagag 18
Db 2 agagagagagagagagag 19

```

```

RESULT 12
US-10-109-624-36
; Sequence 36, Application US/10109624
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Yang, Meijia

```

```

; Knight, James
; Kalbfleisch, Theodore
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
; PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN
; POPULATIONS
; AND IDENTIFICATION OF INHIBITORS OF THESE
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pemle & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,624
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/874,825
; FILING DATE: 13-JUN-1997
; APPLICATION NUMBER: 08/663,824
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-109-624-36

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```

Query Match      100.0%; Score 18; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 agagagagagagagagag 18
Db 2 AGAGAGAGAGAGAGAGAG 19

```

```

RESULT 13
US-10-082-894-7
; Sequence 7, Application US/10082894
; GENERAL INFORMATION:
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Williams, Deryck Jeremy
; APPLICANT: Salmon, Brandy Leigh
; APPLICANT: Bradley, John D.
; TITLE OF INVENTION: NEMATOIDE PGM-LIKE SEQUENCES
; FILE REFERENCE: 12557-003001
; CURRENT APPLICATION NUMBER: US/10/082,894
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US 60/271,781
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7

```

; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Universal primer to poly A tail
US-10-082-894-7

Query Match 100.0%; Score 18; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
| | | | | | | | | | | | | | | | | |
Db 2 agagagagagagagagag 19

Search completed: August 25, 2002, 00:45:46
Job time: 12373 sec

RESULT 14
US-10-160-362-14
; Sequence 14, Application US/10160362
; GENERAL INFORMATION:
; APPLICANT: Williams, Deryck Jeremy
; APPLICANT: Salmon, Brandy
; APPLICANT: Kloeck, Andrew
; TITLE OF INVENTION: NEMATODE ATP SYNTHASE SUBUNIT E-LIKE SEQUENCES
; FILE REFERENCE: 12557-006001
; CURRENT APPLICATION NUMBER: US/10/160,362
; CURRENT FILING DATE: 2002-05-30
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-160-362-14

Query Match 100.0%; Score 18; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | | | | | | | | | | | | | | |
Db 2 agagagagagagagagag 19

RESULT 15
US-10-078-757B-36
; Sequence 36, Application US/10078757B
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F., III
; APPLICANT: RADER, Christoph
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0 Con1
; CURRENT APPLICATION NUMBER: US/10/078,757B
; CURRENT FILING DATE: 2002-02-19
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PCR Primer
US-10-078-757B-36

GenCore version 4.5
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OM nucleic - nucleic search, using sw model.

Run on: August 25, 2002, 00:32:26 ; Search time 8635 Seconds
(without alignments)
45.099 Million cell updates/sec

Title: US-10-077-383-33
Perfect score: 18
Sequence: 1 nnnnnnnnnnnnnnnnn 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /cgn2_6/ptodata/2/pna/US06008_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US06009_COMB.seq:*
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73: /cgn2_6/ptodata/2/pna/US06034_COMB.seq:*

74: /cgn2_6/ptodata/2/pna/US06035_COMB.seq:*

75: /cgn2_6/ptodata/2/pna/US06036_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	0	0.0	1	1	Sequence 702, App
3	0	0.0	1	4	US-08-068-298-17
4	0	0.0	1	4	Sequence 17, Appl
5	0	0.0	1	4	US-08-068-298-17
6	0	0.0	1	5	US-08-154-792A-9
7	0	0.0	1	5	Sequence 9, Appl1
8	0	0.0	1	5	US-08-154-792A-9
9	0	0.0	1	5	Sequence 9, Appl1
10	0	0.0	1	5	US-08-154-792A-24
11	0	0.0	1	5	Sequence 24, Appl
12	0	0.0	1	5	US-08-163-449A-9
13	0	0.0	1	5	Sequence 9, Appl1
14	0	0.0	1	5	US-08-163-449A-24
15	0	0.0	1	6	Sequence 24, Appl
16	0	0.0	1	6	US-08-208-572-10
17	0	0.0	1	6	Sequence 24, Appl
18	0	0.0	1	6	US-08-208-572-10
19	0	0.0	1	6	Sequence 10, Appl
20	0	0.0	1	6	US-08-237-431-6868
21	0	0.0	1	6	Sequence 8868, Ap
22	0	0.0	1	6	US-08-296-757B-7984
23	0	0.0	1	6	Sequence 7984, Ap
24	0	0.0	1	15	US-09-177-650-79
25	0	0.0	1	15	Sequence 79, Appl
26	0	0.0	1	17	US-09-306-333A-121
27	0	0.0	1	17	Sequence 121, App
28	0	0.0	1	17	US-09-306-333A-121
29	0	0.0	1	24	US-09-625-102-323
30	0	0.0	1	24	Sequence 323, App
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32	0	0.0	1	24	Sequence 323, App
33	0	0.0	1	24	US-09-625-102-446
34	0	0.0	1	24	Sequence 446, App
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40	0	0.0	1	24	Sequence 589, App
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42	0	0.0	1	24	Sequence 603, App
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44	0	0.0	1	24	Sequence 603, App
45	0	0.0	1	24	US-09-625-102-614
46	0	0.0	1	24	Sequence 614, App

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 c 38 0 0.0 1 24 US-09-625-102-982
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 c 43 0 0.0 1 24 US-09-634-306B-51773
 c 44 0 0.0 1 24 US-09-634-306B-51773
 c 45 0 0.0 1 24 US-09-634-306B-51841

Sequence 614, App
 Sequence 836, App
 Sequence 836, App
 Sequence 895, App
 Sequence 895, App
 Sequence 982, App
 Sequence 982, App
 Sequence 1048, App
 Sequence 1048, App
 Sequence 1352, App
 Sequence 1352, App
 Sequence 51773, A
 Sequence 51773, A
 Sequence 51841, A

ALIGNMENTS

RESULT 1
 PCT-US93-00977-702
 ; Sequence 702, Application PC/TUS9300977
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
 ; NUMBER OF SEQUENCES: 711
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson, and Bear
 ; STREET: 620 Newport Center Dr. Sixteenth Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/00977
 ; FILING DATE: 19930129
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Altman, Daniel E.
 ; REGISTRATION NUMBER: 34,115
 ; REFERENCE/DOCKET NUMBER: HITACHI.006H
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 714-760-0404
 ; TELEFAX: 714-760-9502
 ; INFORMATION FOR SEQ ID NO: 702:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; PCT-US93-00977-702

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 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 n 1
 Db 1 A 1

Query Match 0.0%; Score 0; DB 1; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 n 1
 Db 1 A 1

RESULT 2
 PCT-US93-00977-702/c
 ; Sequence 702, Application PC/TUS9300977
 ; GENERAL INFORMATION:

; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
 ; NUMBER OF SEQUENCES: 711
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson, and Bear
 ; STREET: 620 Newport Center Dr. Sixteenth Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/00977
 ; FILING DATE: 19930129
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Altman, Daniel E.
 ; REGISTRATION NUMBER: 34,115
 ; REFERENCE/DOCKET NUMBER: HITACHI.006H
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 714-760-0404
 ; TELEFAX: 714-760-9502
 ; INFORMATION FOR SEQ ID NO: 702:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; PCT-US93-00977-702

Query Match 0.0%; Score 0; DB 1; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 n 1
 Db 1 T 1

RESULT 3
 US-08-068-298-17
 ; Sequence 17, Application US/08068298
 ; GENERAL INFORMATION:
 ; APPLICANT: MUENCHAU, DARYL, ET AL.
 ; TITLE OF INVENTION: METHOD FOR GENERATING APTAMERS OF
 ; NON-PREDETERMINED OR SUBSTANTIALLY
 ; TITLE OF INVENTION: NON-PREDETERMINED SEQUENCES
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LYON & LYON
 ; STREET: 611 West Sixth St.
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90017
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/068,298
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/659,980

; FILING DATE: February 21, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CONSALVI, MARY S
; REGISTRATION NUMBER: 32,212
; REFERENCE/DOCKET NUMBER: 193/051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; FEATURE:
; OTHER INFORMATION: where N also may be isoguanine or
; isocytosine
; US-08-068-298-17

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 G 1

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US-08-068-298-17/c
; Sequence 17, Application US/08068298
; GENERAL INFORMATION:
; APPLICANT: MUENCHAU, DARYL, ET AL.
; TITLE OF INVENTION: METHOD FOR GENERATING APTAMERS OF
; TITLE OF INVENTION: NON-PREDETERMINED OR SUBSTANTIALLY
; TITLE OF INVENTION: NON-PREDETERMINED SEQUENCES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 611 West Sixth St.
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,298
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/659,980
; FILING DATE: February 21, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CONSALVI, MARY S
; REGISTRATION NUMBER: 32,212
; REFERENCE/DOCKET NUMBER: 193/051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; FEATURE:

; OTHER INFORMATION: where N also may be isoguanine or
; isocytosine
; US-08-068-298-17

Query Match 0.0%; Score 0; DB 4; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 C 1

RESULT 5
US-08-154-792A-9
; Sequence 9, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.
; APPLICANT: Reenan, Robert A.G.
; APPLICANT: Fishel, Richard
; TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-9

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 A 1

RESULT 6
US-08-154-792A-9/c
; Sequence 9, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.

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; APPLICANT: Reenan, Robert A.G.
; APPLICANT: Fishel, Richard
; TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
; AND Uses Therefor
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-9

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Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 n 1
Db 1 T 1

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RESULT 7
US-08-154-792A-24
; Sequence 24, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.
; APPLICANT: Reenan, Robert A.G.
; APPLICANT: Fishel, Richard
; TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
; AND Uses Therefor
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-24

```

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Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 n 1
Db 1 A 1

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RESULT 8
US-08-154-792A-24/c
; Sequence 24, Application US/08154792A
; GENERAL INFORMATION:
; APPLICANT: Kolodner, Richard D.
; APPLICANT: Reenan, Robert A.G.
; APPLICANT: Fishel, Richard
; TITLE OF INVENTION: Mismatch Repair Genes, Gene Products,
; AND Uses Therefor
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,792A
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-792A-24

```

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 T 1

RESULT 9
 US-08-163-449A-9
 ; Sequence 9, Application US/08163449A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kolodner, Richard D.
 ; APPLICANT: Reenan, Robert A.G.
 ; APPLICANT: Fishel, Richard
 ; TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 ; TITLE OF INVENTION: PRODUCTS,
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/163,449A
 ; FILING DATE: 07-DEC-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Resnick, David S.
 ; REGISTRATION NUMBER: 34,234
 ; REFERENCE/DOCKET NUMBER: 44824-CIP-2
 ; TELEPHONE: (617) 523-3400
 ; TELEFAX: (617) 523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-163-449A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 A 1

RESULT 10
 US-08-163-449A-9/c
 ; Sequence 9, Application US/08163449A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kolodner, Richard D.
 ; APPLICANT: Reenan, Robert A.G.
 ; APPLICANT: Fishel, Richard

; TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 ; TITLE OF INVENTION: PRODUCTS,
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/163,449A
 ; FILING DATE: 07-DEC-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Resnick, David S.
 ; REGISTRATION NUMBER: 34,234
 ; REFERENCE/DOCKET NUMBER: 44824-CIP-2
 ; TELEPHONE: (617) 523-3400
 ; TELEFAX: (617) 523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-163-449A-9

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 T 1

RESULT 11
 US-08-163-449A-24
 ; Sequence 24, Application US/08163449A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kolodner, Richard D.
 ; APPLICANT: Reenan, Robert A.G.
 ; APPLICANT: Fishel, Richard
 ; TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
 ; TITLE OF INVENTION: PRODUCTS,
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/163,449A
FILING DATE: 07-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,234
REFERENCE/DOCKET NUMBER: 44824-CIP-2
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-163-449A-24

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 A 1

RESULT 12

US-08-163-449A-24/c
Sequence 24, Application US/08163449A
GENERAL INFORMATION:
APPLICANT: Kolodner, Richard D.
APPLICANT: Reenan, Robert A.G.
APPLICANT: Fishel, Richard
TITLE OF INVENTION: MISMATCH REPAIR GENES, GENE
TITLE OF INVENTION: PRODUCTS,
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
ADDRESSEE: ROBERTS & CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/163,449A
FILING DATE: 07-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,234
REFERENCE/DOCKET NUMBER: 44824-CIP-2
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-163-449A-24

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 T 1

RESULT 13

US-08-208-572-10
Sequence 10, Application US/08208572
GENERAL INFORMATION:
APPLICANT: Silberstein Ph.D., David S.
APPLICANT: Balcewicz-Sablinska M.D., Maria K.
APPLICANT: Newman Ph.D., Gale W.
TITLE OF INVENTION: CONTROL OF HIV GROWTH WITH ECEF AND
TITLE OF INVENTION: ECEF
TITLE OF INVENTION: DERIVATIVES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHORTE, HALL, & STEWART
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,572
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan Esq., Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: 092662-002
TELEPHONE: (617) 227-5020
TELEFAX: (617) 227-7566
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-208-572-10

Query Match 0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 A 1

RESULT 14

US-08-208-572-10/c
Sequence 10, Application US/08208572
GENERAL INFORMATION:
APPLICANT: Silberstein Ph.D., David S.
APPLICANT: Balcewicz-Sablinska M.D., Maria K.
APPLICANT: Newman Ph.D., Gale W.
TITLE OF INVENTION: CONTROL OF HIV GROWTH WITH ECEF AND

```

; TITLE OF INVENTION: ECF
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL, & STEWART
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,572
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan Esq., Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: 092662-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-5020
; TELEFAX: (617) 227-7566
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-208-572-10

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```

Query Match          0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 n 1
Db 1 T 1

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RESULT 15
US-08-237-491-6868
; Sequence 6868, Application US/08237491
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey
; APPLICANT: Delegeane, Angelo
; APPLICANT: Jernigan, Colleen
; APPLICANT: Levine, Wendy B.
; TITLE OF INVENTION: SHEAR-STRESSED HUMAN UMBILICAL VEIN
; TITLE OF INVENTION: ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 7326
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,491
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/137,951
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,801
; FILING DATE: 17-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8135-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 6868:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: Z-068903
; US-08-237-491-6868

```

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Query Match          0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 n 1
Db 1 C 1

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Search completed: August 25, 2002, 00:32:26
Job time: 16384 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model.

Run on: August 25, 2002, 00:45:46 ; Search time 787.61 seconds
(without alignments)
62.364 Million cell updates/sec

Title: US-10-077-383-33

Perfect score: 18

Sequence: 1 nnnnnnnnnnnnnnnnn 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1737567 seqs, 1364410299 residues

Total number of hits satisfying chosen parameters: 3475134

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New.*

1: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*

2: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*

3: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*

4: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*

5: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*

6: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq.*

7: /cgn2_6/ptodata/2/pna/US12_NEW_COMB.seq.*

8: /cgn2_6/ptodata/2/pna/US13_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	1	7	US-10-027-632-51773
2	0	0.0	1	7	US-10-027-632-51773
3	0	0.0	1	7	US-10-027-632-51773
4	0	0.0	1	7	US-10-027-632-51841
5	0	0.0	1	7	US-10-027-632-51841
6	0	0.0	1	7	US-10-027-632-52001
7	0	0.0	1	7	US-10-027-632-52001
8	0	0.0	1	7	US-10-027-632-52051
9	0	0.0	1	7	US-10-027-632-52051
10	0	0.0	1	7	US-10-027-632-52156
11	0	0.0	1	7	US-10-027-632-52156
12	0	0.0	1	7	US-10-027-632-52157
13	0	0.0	1	7	US-10-027-632-52177
14	0	0.0	1	7	US-10-027-632-52177
15	0	0.0	1	7	US-10-027-632-52215
16	0	0.0	1	7	US-10-027-632-52215
17	0	0.0	1	7	US-10-027-632-52240
18	0	0.0	1	7	US-10-027-632-52240
19	0	0.0	1	7	US-10-027-632-52272
20	0	0.0	1	7	US-10-027-632-52272
21	0	0.0	1	7	US-10-027-632-52624
22	0	0.0	1	7	US-10-027-632-52624
23	0	0.0	1	7	US-10-027-632-52642
24	0	0.0	1	7	US-10-027-632-52642
25	0	0.0	1	7	US-10-027-632-52668

c	26	0	0.0	1	7	US-10-027-632-52668	Sequence 52668, A
c	27	0	0.0	1	7	US-10-027-632-52677	Sequence 52677, A
c	28	0	0.0	1	7	US-10-027-632-52677	Sequence 52677, A
c	29	0	0.0	1	7	US-10-027-632-52707	Sequence 52707, A
c	30	0	0.0	1	7	US-10-027-632-52707	Sequence 52707, A
c	31	0	0.0	1	7	US-10-027-632-52714	Sequence 52714, A
c	32	0	0.0	1	7	US-10-027-632-52714	Sequence 52714, A
c	33	0	0.0	1	7	US-10-027-632-52721	Sequence 52721, A
c	34	0	0.0	1	7	US-10-027-632-52721	Sequence 52721, A
c	35	0	0.0	1	7	US-10-027-632-52776	Sequence 52776, A
c	36	0	0.0	1	7	US-10-027-632-52776	Sequence 52776, A
c	37	0	0.0	1	7	US-10-027-632-52863	Sequence 52863, A
c	38	0	0.0	1	7	US-10-027-632-52863	Sequence 52863, A
c	39	0	0.0	1	7	US-10-027-632-52864	Sequence 52864, A
c	40	0	0.0	1	7	US-10-027-632-52864	Sequence 52864, A
c	41	0	0.0	1	7	US-10-027-632-52891	Sequence 52891, A
c	42	0	0.0	1	7	US-10-027-632-52891	Sequence 52891, A
c	43	0	0.0	1	7	US-10-027-632-52890	Sequence 52890, A
c	44	0	0.0	1	7	US-10-027-632-52890	Sequence 52890, A
c	45	0	0.0	1	7	US-10-027-632-58459	Sequence 58459, A

ALIGNMENTS

RESULT 1
US-10-027-632-51773
; Sequence 51773, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51773
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51773

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 c 1

RESULT 2

US-10-027-632-51773/c
; Sequence 51773, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51773
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51773

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 G 1

RESULT 3
US-10-027-632-51841
; Sequence 51841, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51841
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51841

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 Y 1
RESULT 4
US-10-027-632-51841/c
; Sequence 51841, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51841
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51841

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 R 1

RESULT 5
US-10-027-632-52001
; Sequence 52001, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52001
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52001

Query Match 0.0% Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 y 1

RESULT 6

US-10-027-632-52001/c
; Sequence 52001, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52001
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52001

Query Match 0.0% Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 r 1

RESULT 7

US-10-027-632-52051
; Sequence 52051, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52051
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52051

Query Match 0.0% Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

RESULT 8

US-10-027-632-52051/c
; Sequence 52051, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52051
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52051

Query Match 0.0% Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 G 1

RESULT 9

US-10-027-632-52156
; Sequence 52156, Application US/10027632
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52156
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52156

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 c 1

RESULT 10
US-10-027-632-52156/c
; Sequence 52156, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52156
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52156

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 n 1
Db 1 g 1

RESULT 11
US-10-027-632-52157
; Sequence 52157, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52157
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52157

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 c 1

RESULT 12
US-10-027-632-52157/c
; Sequence 52157, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52157
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52157

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 G 1

RESULT 13

US-10-027-632-52177
; Sequence 52177, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52177
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52177

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

RESULT 14

US-10-027-632-52177/c
; Sequence 52177, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52177
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52177

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 G 1

RESULT 15

US-10-027-632-52215
; Sequence 52215, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52215
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52215

Query Match 0.0%; Score 0; DB 7; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

Search completed: August 25, 2002, 00:45:46

Mon Aug 26 10:18:22 2002

us-10-077-383-33.rnpn

Page 6

Job time: 12373 sec

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Query Match      0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
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Db 1 N 1

RESULT 2
A95992/c A95992 1 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 25 from Patent WO9924578.
ACCESSION A95992
VERSION A95992.1 GI:6779888
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 25 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
source
Location/Qualifiers
1
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 0 c 0 g 0 t 1 others
ORIGIN

Query Match      0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
   |
Db 1 N 1

RESULT 3
A96002/c A96002 1 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 35 from Patent WO9924578.
ACCESSION A96002
VERSION A96002.1 GI:6779893
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 35 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
source
Location/Qualifiers
1
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 0 c 0 g 0 t 1 others
ORIGIN

Query Match      0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
   |
Db 1 N 1

RESULT 6
A96012/c A96012 1 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 45 from Patent WO9924578.
ACCESSION A96012
VERSION A96012.1 GI:6779898
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 45 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
source
Location/Qualifiers
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/db_xref="taxon:32644"
BASE COUNT 0 a 0 c 0 g 0 t 1 others
ORIGIN

Query Match      0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
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Db 1 N 1

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Db 1 N 1

RESULT 4
A96002/c A96002 1 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 35 from Patent WO9924578.
ACCESSION A96002
VERSION A96002.1 GI:6779893
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 35 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
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Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 0 c 0 g 0 t 1 others
ORIGIN

Query Match      0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
   |
Db 1 N 1

RESULT 5
A96012/c A96012 1 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 45 from Patent WO9924578.
ACCESSION A96012
VERSION A96012.1 GI:6779898
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 45 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
source
Location/Qualifiers
1
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 0 c 0 g 0 t 1 others
ORIGIN

Query Match      0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
   |
Db 1 N 1

RESULT 6
A96012/c A96012 1 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 45 from Patent WO9924578.

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ACCESSION A96012
VERSION A96012.1 GI:6779898

KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1)

AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.

TITLE Neisserial antigens

JOURNAL Patent: WO 924578-A 45 20-MAY-1999;

PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);

CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

FEATURES
source

BASE COUNT 0 a 0 c 0 g 0 t 1 others
ORIGIN /db_xref="taxon:32644"

Query Match 0.0%; Score 0; DB 6; Length 1;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1

Db 1 n 1

RESULT 7

A96022

LOCUS A96022

DEFINITION Sequence 55 from Patent WO924578.

ACCESSION A96022

VERSION A96022.1 GI:6779903

KEYWORDS

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1)

AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.

TITLE Neisserial antigens

JOURNAL Patent: WO 924578-A 55 20-MAY-1999;

PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);

CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

FEATURES
source

BASE COUNT 0 a 0 c 0 g 0 t 1 others
ORIGIN /db_xref="taxon:32644"

Query Match 0.0%; Score 0; DB 6; Length 1;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1

Db 1 n 1

RESULT 8

A96022/c

LOCUS A96022

DEFINITION Sequence 55 from Patent WO924578.

ACCESSION A96022

VERSION A96022.1 GI:6779903

KEYWORDS

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1)

AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 924578-A 55 20-MAY-1999;

PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);

CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

FEATURES
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BASE COUNT 0 a 0 c 0 g 0 t 1 others
ORIGIN /db_xref="taxon:32644"

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1

Db 1 n 1

RESULT 9

A96040

LOCUS A96040

DEFINITION Sequence 73 from Patent WO924578.

ACCESSION A96040

VERSION A96040.1 GI:6779912

KEYWORDS

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1)

AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.

TITLE Neisserial antigens

JOURNAL Patent: WO 924578-A 73 20-MAY-1999;

PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);

CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

FEATURES
source

BASE COUNT 0 a 0 c 0 g 0 t 1 others
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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1

Db 1 n 1

RESULT 10

A96040/c

LOCUS A96040

DEFINITION Sequence 73 from Patent WO924578.

ACCESSION A96040

VERSION A96040.1 GI:6779912

KEYWORDS

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1)

AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.

TITLE Neisserial antigens

JOURNAL Patent: WO 924578-A 73 20-MAY-1999;

PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);

CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

FEATURES
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BASE COUNT 0 a 0 c 0 g 0 t 1 others
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BASE COUNT
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
|
Db 1 N 1

RESULT 11
A96058 LOCUS A96058 1 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 91 from Patent WO9924578.
ACCESSION A96058
VERSION A96058.1 GI:6779921
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 91 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
source
1
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
0 a 0 c 0 g 0 t 1 others

BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
|
Db 1 N 1

RESULT 12
A96058/c LOCUS A96058 1 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 91 from Patent WO9924578.
ACCESSION A96058
VERSION A96058.1 GI:6779921
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 91 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
source
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Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
0 a 0 c 0 g 0 t 1 others

BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
|
Db 1 N 1

RESULT 13
A96076 LOCUS A96076 1 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 109 from Patent WO9924578.
ACCESSION A96076
VERSION A96076.1 GI:6779930
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 109 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
source
1
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
0 a 0 c 0 g 0 t 1 others

BASE COUNT
ORIGIN

Query Match 0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
|
Db 1 N 1

RESULT 14
A96076/c LOCUS A96076 1 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 109 from Patent WO9924578.
ACCESSION A96076
VERSION A96076.1 GI:6779930
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 109 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
source
1
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
0 a 0 c 0 g 0 t 1 others

BASE COUNT
ORIGIN

Query Match 0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
|
Db 1 N 1
```



```

RESULT 15
A96086
LOCUS       A96086               1 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION   Sequence 119 from Patent WO924578.
ACCESSION   A96086
VERSION     A96086.1  GI:6779935
KEYWORDS    .
SOURCE      .
  ORGANISM   unidentified.
             unclassified.
REFERENCE   1 (bases 1 to 1)
  AUTHORS   Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
  TITLE     Neisserial antigens
  JOURNAL   Patent: WO 924578-A 119 20-MAY-1999;
            PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
            CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES    Location/Qualifiers
             source
               1
               /organism="unidentified"
               /db_xref="taxon:32644"
BASE COUNT   0 a      0 c      0 g      0 t      1 others
ORIGIN

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Query Match      0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

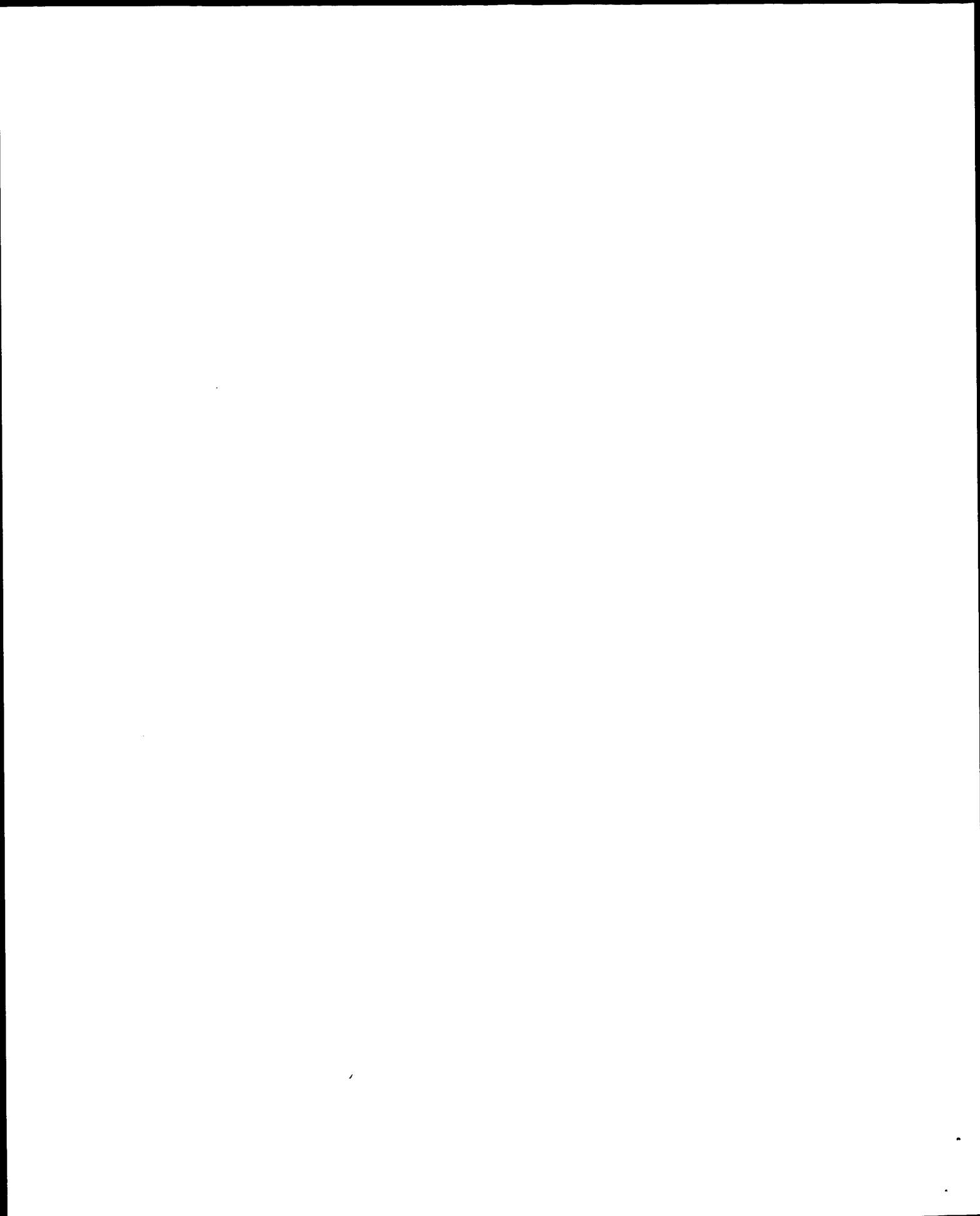
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Qy  1 n 1
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Db  1 n 1

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Job time: 22406 sec



PT Nucleic acid encoding potassium channels KCNQ2 and 3
 XX Claim 65; Page 151; 195pp; English.

CC This invention describes novel human and mouse potassium channel
 CC proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode
 CC KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for
 CC diagnosis and prognosis of benign familial neonatal epilepsy (BFNE),
 CC juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or
 CC transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the
 CC proteins themselves in cell-free form) are used to screen for agents that
 CC can be used to treat or prevent these forms of epilepsy. Fragments of the
 CC encoding nucleic acids are used as probes or primers, either for
 CC detecting mutations or for isolation of related sequences, while the
 CC complete sequences may be used in gene therapy to provide wild-type
 CC protein. Antibodies specific for mutant or wild-type proteins are used
 CC as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins
 CC are useful in rational design of drugs and therapeutically (in
 CC replacement therapies). The forms of epilepsy associated with mutations
 CC in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are
 CC manifest), and better treatment options will be available.
 CC AAX57074-X57139 are primers used in the method of the invention.

XX Sequence 1 BP; 1 A; 0 C; 0 G; 0 U; 0 other;
 SQ

Query Match 0.0%; Score 0; DB 20; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
 Db 1 a 1

RESULT 2
 AAX57131/C
 ID AAX57131 standard; DNA; 1 BP.

XX AAX57131;
 XX 22-JUL-1999 (first entry)

XX Human mutant KCNQ3 primer 26.

XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
 KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
 KW detection; gene therapy; drug screening; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9921875-A1.

XX 06-MAY-1999.

XX 23-OCT-1998; 98WO-US22375.

XX 24-OCT-1997; 97US-0063147.

XX (UTAH) UNIV UTAH RES FOUND.

XX Charlier C, Leppert MF, Singh NA;

XX WPI; 1999-312938/26.

XX Nucleic acid encoding potassium channels KCNQ2 and 3

XX Claim 65; Page 151; 195pp; English.

XX This invention describes novel human and mouse potassium channel
 CC proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode

CC KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for
 CC diagnosis and prognosis of benign familial neonatal epilepsy (BFNE),
 CC juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or
 CC transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the
 CC proteins themselves in cell-free form) are used to screen for agents that
 CC can be used to treat or prevent these forms of epilepsy. Fragments of the
 CC encoding nucleic acids are used as probes or primers, either for
 CC detecting mutations or for isolation of related sequences, while the
 CC complete sequences may be used in gene therapy to provide wild-type
 CC protein. Antibodies specific for mutant or wild-type proteins are used
 CC as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins
 CC are useful in rational design of drugs and therapeutically (in
 CC replacement therapies). The forms of epilepsy associated with mutations
 CC in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are
 CC manifest), and better treatment options will be available.
 CC AAX57074-X57139 are primers used in the method of the invention.

XX Sequence 1 BP; 1 A; 0 C; 0 G; 0 U; 0 other;
 SQ

Query Match 0.0%; Score 0; DB 20; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
 Db 1 t 1

RESULT 3
 AAN80743
 ID AAN80743 standard; DNA; 3 BP.

XX AAN80743;
 XX 10-SEP-1990 (first entry)

XX Sequence encoding complete mature and precursor forms of human tissue
 DE factor heavy chain proteins (huTFh & pre-huTFh, respectively).

XX Human tissue factor heavy chain (huTFh); immunoassays;
 KW precursor human tissue factor heavy chain (pre-huTFh);
 KW human tissue factor detection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 34..921

FT /*tag= a

FT /product=pre-huTF

FT mat_peptide 130..921

FT /*tag= b

FT /product=huTFh

XX WO8807543-A.

XX 06-OCT-1988.

XX 29-MAR-1988; 88WO-US000998.

XX 25-JUN-1987; 87US-0067103.

XX (SCRI-) SCRIPPS CLINIC RES.

XX Eddington TS, Morrissey JH;

XX WPI; 1988-292837/41.

XX P-PSDB; AAP80713.

XX New DNA segment -

XX PT has gene encoding human tissue factor heavy chain protein and is
 PT useful for inhibiting coagulation

PS Disclosure; ; pp: English.

XX A DNA segment with a nucleotide sequence from about 130 to about 918 of
 CC the sequence given here is claimed. Also claimed are antibodies which
 CC immunoreact with hutfh and the claimed peptides (given in AAP80713).
 CC The antibodies may be used in immunoassays for detection of hutfh. The
 CC claimed peptides may be used to inhibit the binding of hutfh to
 CC coagulation factor VII/VIIa in vivo.

XX Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 9; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
 Db 1 n 1

RESULT 4
 AAN80743/C
 ID AAN80743 standard; DNA; 3 BP.
 AC AAN80743;
 XX 10-SEP-1990 (first entry)
 XX
 XX Sequence encoding complete mature and precursor forms of human tissue
 DE factor heavy chain proteins (hutfh & pre-hutfh, respectively).
 DE
 XX Human tissue factor heavy chain (hutfh); immunoassays;
 KW precursor human tissue factor heavy chain (pre-hutfh);
 KW human tissue factor detection.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH 34..921
 FT CDS /*tag= a
 FT /product=pre-hutfh
 FT mat_peptide 130..921
 FT /*tag= b
 FT /product=hutfh

XX WO8807543-A.
 XX 06-OCT-1988.
 XX 29-MAR-1988; 88WO-US00998.
 XX 25-JUN-1987; 87US-0067103.
 XX (SCRI-) SCRIPPS CLINTC RES.
 XX Eddington TS, Morrissey JH;
 XX WPI: 1988-292837/41.
 XX P-PSDB; AAP80713.

XX New DNA segment -
 PT has gene encoding human tissue factor heavy chain protein and is
 PT useful for inhibiting coagulation

XX Disclosure; ; pp: English.

XX A DNA segment with a nucleotide sequence from about 130 to about 918 of
 CC the sequence given here is claimed. Also claimed are antibodies which
 CC immunoreact with hutfh and the claimed peptides (given in AAP80713).
 CC The antibodies may be used in immunoassays for detection of hutfh. The
 CC claimed peptides may be used to inhibit the binding of hutfh to
 CC coagulation factor VII/VIIa in vivo.

XX SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 9; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
 Db 3 N 3

RESULT 5
 AAQ85491
 ID AAQ85491 standard; cDNA; 3 BP.
 XX
 XX AAQ85491;
 XX 18-AUG-1995 (first entry)
 XX Plasmid pEZZ318.thy2.
 XX OMTKY3; turkey ovomucoid third domain peptide inhibitor;
 KW furin inhibitor; protease inhibitor; pEZZ318.thy2; probe;
 KW Escherichia coli; ss.
 XX Synthetic.

XX WO9502055-A.
 XX 19-JAN-1995.
 XX 08-JUL-1994; 94WO-US07779.
 XX 09-JUL-1993; 93US-0089248.
 XX (ANDE/) ANDERSON S.
 PA (LASK/) LASKOWSKI M.
 PI Anderson S, Laskowski M;
 XX WPI: 1995-066900/09.

PT Protein inhibitors of serine proteinase(s), e.g. furin, deriv.
 PT from turkey ovomucoid third domain - used as laboratory reagents
 PT to study the proteinase(s), or as chemotherapeutic agents to
 PT treat diseases associated with them

XX Disclosure; Page 42-45; 66pp; English.

XX In synthetic analogs of turkey ovomucoid domain protein (6-56)
 CC (OMTKY3), given in AAR69818-24, the region immediately adjacent to
 CC the reactive site peptide bond is mutated to include the consensus
 CC sequence of furin or other serine protease. Polynucleotides
 CC encoding such analogs are incorporated into pEZZ318.thy2 and
 CC expressed in Escherichia coli RV308 (ATCC 31608).

XX Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 16; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
 Db 1 n 1

RESULT 6
 AAQ85491/C
 ID AAQ85491 standard; cDNA; 3 BP.

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XX AC AAQ85491;
XX DT 18-AUG-1995 (first entry)
XX DE Plasmid PEZ3318.thy2.
XX KW OMTK3; turkey ovomucoid third domain peptide inhibitor;
XX KW furin inhibitor; protease inhibitor; PEZ3318.thy2; probe;
XX KW Escherichia coli; ss.
XX OS Synthetic.
XX PN WO9502055-A.
XX PD 19-JAN-1995.
XX PF 08-JUL-1994; 94WO-US07779.
XX PR 09-JUL-1993; 93US-0089248.
XX PA (ANDE/) ANDERSON S.
XX PA (LASK/) LASKOWSKI M.
XX PI Anderson S, Laskowski M;
XX DR WPI; 1995-066900/09.
XX PT Protein inhibitors of serine proteinase(s), e.g. furin, deriv.
XX PT from turkey ovomucoid third domain - used as laboratory reagents
XX PT to study the proteinase(s), or as chemotherapeutic agents to
XX PT treat diseases associated with them
XX PS Disclosure; Page 42-45; 66pp; English.
XX CC In synthetic analogs of turkey ovomucoid domain protein (6-56)
XX CC (OMTKY3), given in AAR69818-24, the region immediately adjacent to
XX CC the reactive site peptide bond is mutated to include the consensus
XX CC sequence of furin or other serine protease. Polynucleotides
XX CC encoding such analogs are incorporated into PEZ3318.thy2 and
XX CC expressed in Escherichia coli RV308 (ATCC 31608).
XX SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 16; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
DB 3 N 3

RESULT 7
AAT33326
ID AAT33326 standard; RNA; 3 BP.
XX AC AAT33326;
XX DT 12-NOV-1996 (first entry)
XX DE CAPL trinucleotide.
XX KW CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
XX KW osteosarcoma; therapy; ss.
XX OS Synthetic.
XX PN WO9625499-A1.
XX PD 22-AUG-1996.
XX PF 16-FEB-1996; 96WO-US02108.
XX PR 17-FEB-1995; 95US-0391375.
XX PA (HYBR-) HYBRIDON INC.
XX PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX PI Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
XX PI Von Hofe E;
XX DR WPI; 1996-393400/39.
XX PT Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
XX PT useful to inhibit metastatic cancer, partic. osteosarcoma
XX PS Claim 2; Page 56; 70pp; English.
XX

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PF 16-FEB-1996; 96WO-US02108.
XX
PR 17-FEB-1995; 95US-0391375.
XX
PA (HYBR-) HYBRIDON INC.
XX
PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX
PI Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
PI Von Hofe E;
XX
DR WPI; 1996-393400/39.
XX
PT Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
PT useful to inhibit metastatic cancer, partic. osteosarcoma
XX
PS Claim 2; Page 56; 70pp; English.
XX
CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
CC expression may include the trinucleotide GUC (AAT33326, given in 5',
CC to 3' direction) found in codon 14 of CAPL mRNA. These and
CC other antisense oligonucleotides (AAT33327-36) complementary to
CC specific regions of the CAPL gene (see also AAT33345), as well as
CC CAPL-specific ribozymes (AAT3337-40) can be administered to a
CC patient as a means of inhibiting metastatic cancer.
XX
SQ Sequence 3 BP; 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 17; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
DB 1 c 1

RESULT 8
AAT33326/c
ID AAT33326 standard; RNA; 3 BP.
XX AC AAT33326;
XX DT 12-NOV-1996 (first entry)
XX DE CAPL trinucleotide.
XX KW CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
XX KW osteosarcoma; therapy; ss.
XX OS Synthetic.
XX PN WO9625499-A1.
XX PD 22-AUG-1996.
XX PF 16-FEB-1996; 96WO-US02108.
XX PR 17-FEB-1995; 95US-0391375.
XX PA (HYBR-) HYBRIDON INC.
XX PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX PI Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
XX PI Von Hofe E;
XX DR WPI; 1996-393400/39.
XX PT Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
XX PT useful to inhibit metastatic cancer, partic. osteosarcoma
XX PS Claim 2; Page 56; 70pp; English.
XX

```

CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5'
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.
 XX
 SQ Sequence 3 BP; 0 A; 1 C; 1 G; 1 U; 0 other;
 0.0%; Score 0; DB 17; Length 3;
 Query Match 0.0%; Pred. No. 0;
 Best Local Similarity 0.0%; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 0; Conserved 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 n 1
 Db 3 C 3
 RESULT 9
 ID AAA94655 standard; DNA; 3 BP.
 AC AAA94655;
 XX
 XX 15-JAN-2001 (first entry)
 DT Human TUB gene probe #2.
 DE Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;
 KW TUB; ss.
 XX Homo sapiens.
 OS
 XX US6114502-A.
 PN
 XX 05-SEP-2000.
 PD
 XX 27-FEB-1998; 98US-0032365.
 PF
 XX 22-AUG-1996; 96US-0701380.
 PR
 PR 04-SEP-1996; 96US-0706292.
 PR
 PR 10-APR-1996; 96US-0630592.
 PR
 PR 17-SEP-1996; 96US-0714991.
 PR
 PR 30-APR-1997; 97US-0850218.
 PR
 PR 01-AUG-1997; 97US-0904699.
 PR
 PR 17-SEP-1997; 97US-0932306.
 XX
 XX (AXYS-) AXYS PHARM INC.
 XX
 XX North M, Nishina P, Noben-Trauth K, Naggert J;
 PI
 XX WPI; 2000-586483/55.
 DR
 XX Mammalian proteins expressed in retina and brain, useful for producing
 PT antibodies and for diagnosing neurosensory defects including cochlear
 PT degeneration, peripheral retinal degeneration and cone-rod retinal
 PT dystrophy -
 XX
 PS Disclosure; Columns 81-82; 61pp; English.
 XX
 CC The present invention relates to human and murine cDNAs from a
 CC neurosensory defect associated gene family. The novel cDNAs are mouse
 CC tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB
 CC form 6 (see AAA94633), human TUB form 1 (see AAA94637) and
 CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
 CC immunogens to raise antibodies that specifically identify TUB/TULP
 CC expressing cells and in drug screening assays directed at neurosensory
 CC defects. The novel proteins encoded by the present sequence can be used
 CC for the treatment of neurosensory degenerative conditions e.g. retinal
 CC dystrophies. The present sequence is a probe used to isolate the novel
 CC

CC genes of the present invention.
 XX
 SQ Sequence 3 BP; 0 A; 0 C; 3 G; 0 U; 0 other;
 0.0%; Score 0; DB 21; Length 3;
 Query Match 0.0%; Pred. No. 0;
 Best Local Similarity 0.0%; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 0; Conserved 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 n 1
 Db 1 g 1
 RESULT 10
 ID AAA94655 standard; DNA; 3 BP.
 AC AAA94655;
 XX
 XX 15-JAN-2001 (first entry)
 DT Human TUB gene probe #2.
 DE Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;
 KW TUB; ss.
 XX Homo sapiens.
 OS
 XX US6114502-A.
 PN
 XX 05-SEP-2000.
 PD
 XX 27-FEB-1998; 98US-0032365.
 PF
 XX 22-AUG-1996; 96US-0701380.
 PR
 PR 04-SEP-1996; 96US-0706292.
 PR
 PR 10-APR-1996; 96US-0630592.
 PR
 PR 17-SEP-1996; 96US-0714991.
 PR
 PR 30-APR-1997; 97US-0850218.
 PR
 PR 01-AUG-1997; 97US-0904699.
 PR
 PR 17-SEP-1997; 97US-0932306.
 XX
 XX (AXYS-) AXYS PHARM INC.
 XX
 XX North M, Nishina P, Noben-Trauth K, Naggert J;
 PI
 XX WPI; 2000-586483/55.
 DR
 XX Mammalian proteins expressed in retina and brain, useful for producing
 PT antibodies and for diagnosing neurosensory defects including cochlear
 PT degeneration, peripheral retinal degeneration and cone-rod retinal
 PT dystrophy -
 XX
 PS Disclosure; Columns 81-82; 61pp; English.
 XX
 CC The present invention relates to human and murine cDNAs from a
 CC neurosensory defect associated gene family. The novel cDNAs are mouse
 CC tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB
 CC form 6 (see AAA94633), human TUB form 1 (see AAA94637) and
 CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
 CC immunogens to raise antibodies that specifically identify TUB/TULP
 CC expressing cells and in drug screening assays directed at neurosensory
 CC defects. The novel proteins encoded by the present sequence can be used
 CC for the treatment of neurosensory degenerative conditions e.g. retinal
 CC dystrophies. The present sequence is a probe used to isolate the novel
 CC
 SQ Sequence 3 BP; 0 A; 0 C; 3 G; 0 U; 0 other;
 0.0%; Score 0; DB 21; Length 3;
 Query Match 0.0%; Pred. No. 0;
 Best Local Similarity 0.0%; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 0; Conserved 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 n 1
 Db 1 g 1
 RESULT 10
 ID AAA94655 standard; DNA; 3 BP.
 AC AAA94655;
 XX
 XX 15-JAN-2001 (first entry)
 DT Human TUB gene probe #2.
 DE Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;
 KW TUB; ss.
 XX Homo sapiens.
 OS
 XX US6114502-A.
 PN
 XX 05-SEP-2000.
 PD
 XX 27-FEB-1998; 98US-0032365.
 PF
 XX 22-AUG-1996; 96US-0701380.
 PR
 PR 04-SEP-1996; 96US-0706292.
 PR
 PR 10-APR-1996; 96US-0630592.
 PR
 PR 17-SEP-1996; 96US-0714991.
 PR
 PR 30-APR-1997; 97US-0850218.
 PR
 PR 01-AUG-1997; 97US-0904699.
 PR
 PR 17-SEP-1997; 97US-0932306.
 XX
 XX (AXYS-) AXYS PHARM INC.
 XX
 XX North M, Nishina P, Noben-Trauth K, Naggert J;
 PI
 XX WPI; 2000-586483/55.
 DR
 XX Mammalian proteins expressed in retina and brain, useful for producing
 PT antibodies and for diagnosing neurosensory defects including cochlear
 PT degeneration, peripheral retinal degeneration and cone-rod retinal
 PT dystrophy -
 XX
 PS Disclosure; Columns 81-82; 61pp; English.
 XX
 CC The present invention relates to human and murine cDNAs from a
 CC neurosensory defect associated gene family. The novel cDNAs are mouse
 CC tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB
 CC form 6 (see AAA94633), human TUB form 1 (see AAA94637) and
 CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
 CC immunogens to raise antibodies that specifically identify TUB/TULP
 CC expressing cells and in drug screening assays directed at neurosensory
 CC defects. The novel proteins encoded by the present sequence can be used
 CC for the treatment of neurosensory degenerative conditions e.g. retinal
 CC dystrophies. The present sequence is a probe used to isolate the novel
 CC

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
Db 3 C 3

RESULT 11
AAL20244
ID AAL20244 standard; cDNA; 3 BP.
XX
XX AAL20244;
AC
XX 07-DEC-2001 (first entry)
XX
XX Human breast cancer expressed polynucleotide 12701.
XX
XX Human; breast cancer; cell marker; cytostatic; ss.
XX
XX Homo sapiens.
XX
XX WO200151628-A2.
XX
XX 19-JUL-2001.
XX
XX 10-JAN-2001; 2001WO-US00798.
XX
XX 14-JAN-2000; 2000US-0176077.
XX
XX 14-MAR-2000; 2000US-0189167.
XX
XX 24-MAR-2000; 2000US-0192099.
XX
XX 29-MAR-2000; 2000US-0193480.
XX
XX 15-MAY-2000; 2000US-0205230.
XX
XX 09-JUN-2000; 2000US-0211315.
XX
XX 25-JUL-2000; 2000US-0220534.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX
XX WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer -
XX
XX Claim 1; Page 2245; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
XX
XX (AAL07544-AAL26789) and methods of assessing whether a patient is
XX
XX afflicted with breast cancer by examining the correlation between the
XX
XX expression of certain markers and the cancerous state of breast cells.
XX
XX The polynucleotides and encoded polypeptides are potential markers for
XX
XX detecting, diagnosing, monitoring, characterising treating and
XX
XX potentially preventing breast cancer. The polynucleotides and encoded
XX
XX polypeptides are also useful for isolating compounds with cytostatic
XX
XX activity.
XX
XX Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;
XX
XX Claim 1; Page 2245; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
XX
XX (AAL07544-AAL26789) and methods of assessing whether a patient is
XX
XX afflicted with breast cancer by examining the correlation between the
XX
XX expression of certain markers and the cancerous state of breast cells.
XX
XX The polynucleotides and encoded polypeptides are potential markers for
XX
XX detecting, diagnosing, monitoring, characterising treating and
XX
XX potentially preventing breast cancer. The polynucleotides and encoded
XX
XX polypeptides are also useful for isolating compounds with cytostatic
XX
XX activity.
XX
XX Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

Query Match 0.0%; Score 0; DB 22; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
Db 3 A 3

RESULT 13
AAL081664
ID AAL081664 standard; RNA; 4 BP.
XX
XX AAL081664;
AC
XX
XX 29-SEP-1995 (first entry)
XX
XX bFGF binding oligomer core sequence #1.
XX
XX Basic; fibroblast growth factor; bFGF; stem-loop structure;
XX
XX bubble structure; pseudoknot; receptor; heparin; competition;
XX
XX inhibition; enhance; neovascularisation; solid tumour; cancer;
XX
XX metastasis; diagnosis; gene therapy; ss.
XX
XX Synthetic.
XX
XX WO9500528-A.
XX
XX PN

```



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XX PD 05-JAN-1995.
XX PF 17-JUN-1994; 94WO-US06884.
XX PR 18-JUN-1993; 93US-0079677.
XX PR 07-JAN-1994; 94US-0179491.
XX PA (PHAR-) PHARMAGENICS INC.
XX PI Beutel BA, Joesten ME;
XX PS WPI; 1995-051992/07.
XX PT New oligo-nucleotide(s) that bind to basic fibroblast growth
XX factor - modulating, esp. inhibiting, its activity, useful in
XX treating cancer, preventing metastasis, and diagnosis.
XX PS Claim 3; Page 25; 44pp; English.
XX CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
XX the activity of basic fibroblast growth factor (bFGF) by binding
XX to the bFGF protein. Most esp. the sequences given in AAQ81664-67
XX represent core sequences of which at least one is present in each of
XX the binding oligos. These oligonucleotides may form a single
XX strand, double strand, a stem-loop structure, a bubble structure, a
XX pseudoknot or a closed, circular structure. bFGF binds to high
XX affinity receptor and low affinity heparin-like molecules on the
XX cell surface. These oligonucleotides bind to bFGF in competition
XX or enhance the activity of bFGF. Particularly, they inhibit
XX neovascularisation so they can be used to suppress growth of solid
XX tumours and to reduce the risk of metastasis. They can be used as
XX diagnostic reagents to determine the presence of thrombin, or used in
XX gene therapy.
XX SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 16; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
DB 1 g 1

RESULT 14
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ID AAQ81664 standard; RNA; 4 BP.
XX AC AAQ81664;
XX DT 29-SEP-1995 (first entry)
XX DE bFGF binding oligomer core sequence #1.
XX KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
XX bubble structure; pseudoknot; receptor; heparin; competition;
XX inhibition; enhance; neovascularisation; solid tumour; cancer;
XX metastasis; diagnosis; gene therapy; ss.
XX OS Synthetic.
XX PN WO9500528-A.
XX PD 05-JAN-1995.
XX PF 17-JUN-1994; 94WO-US06884.
XX PR 18-JUN-1993; 93US-0079677.
XX PR 07-JAN-1994; 94US-0179491.
XX PA (PHAR-) PHARMAGENICS INC.
XX PI Beutel BA, Joesten ME;
XX PS WPI; 1995-051992/07.
XX PT New oligo-nucleotide(s) that bind to basic fibroblast growth
XX factor - modulating, esp. inhibiting, its activity, useful in
XX treating cancer, preventing metastasis, and diagnosis.
XX PS Claim 3; Page 25; 44pp; English.
XX CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
XX the activity of basic fibroblast growth factor (bFGF) by binding
XX to the bFGF protein. Most esp. the sequences given in AAQ81664-67
XX represent core sequences of which at least one is present in each of
XX the binding oligos. These oligonucleotides may form a single
XX strand, double strand, a stem-loop structure, a bubble structure, a
XX pseudoknot or a closed, circular structure. bFGF binds to high
XX affinity receptor and low affinity heparin-like molecules on the
XX cell surface. These oligonucleotides bind to bFGF in competition
XX or enhance the activity of bFGF. Particularly, they inhibit
XX neovascularisation so they can be used to suppress growth of solid
XX tumours and to reduce the risk of metastasis. They can be used as
XX diagnostic reagents to determine the presence of thrombin, or used in
XX gene therapy.
XX SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

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XX PA (PHAR-) PHARMAGENICS INC.
XX PI Beutel BA, Joesten ME;
XX XX WPI; 1995-051992/07.
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XX neovascularisation so they can be used to suppress growth of solid
XX tumours and to reduce the risk of metastasis. They can be used as
XX diagnostic reagents to determine the presence of thrombin, or used in
XX gene therapy.
XX SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 16; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
DB 4 G 4

RESULT 15
AAQ81665
ID AAQ81665 standard; RNA; 4 BP.
XX AC AAQ81665;
XX DT 29-SEP-1995 (first entry)
XX DE bFGF binding oligomer core sequence #2.
XX KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
XX bubble structure; pseudoknot; receptor; heparin; competition;
XX inhibition; enhance; neovascularisation; solid tumour; cancer;
XX metastasis; diagnosis; gene therapy; ss.
XX OS Synthetic.
XX PN WO9500528-A.
XX PD 05-JAN-1995.
XX PF 17-JUN-1994; 94WO-US06884.
XX PR 18-JUN-1993; 93US-0079677.
XX PR 07-JAN-1994; 94US-0179491.
XX PA (PHAR-) PHARMAGENICS INC.
XX PI Beutel BA, Joesten ME;
XX PS WPI; 1995-051992/07.
XX PT New oligo-nucleotide(s) that bind to basic fibroblast growth
XX factor - modulating, esp. inhibiting, its activity, useful in
XX treating cancer, preventing metastasis, and diagnosis.
XX PS Claim 3; Page 25; 44pp; English.
XX CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
XX the activity of basic fibroblast growth factor (bFGF) by binding
XX to the bFGF protein. Most esp. the sequences given in AAQ81664-67
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XX the binding oligos. These oligonucleotides may form a single
XX strand, double strand, a stem-loop structure, a bubble structure, a
XX pseudoknot or a closed, circular structure. bFGF binds to high
XX affinity receptor and low affinity heparin-like molecules on the
XX cell surface. These oligonucleotides bind to bFGF in competition
XX or enhance the activity of bFGF. Particularly, they inhibit
XX neovascularisation so they can be used to suppress growth of solid
XX tumours and to reduce the risk of metastasis. They can be used as
XX diagnostic reagents to determine the presence of thrombin, or used in
XX gene therapy.
XX SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

```

PT New oligo-nucleotide(s) that bind to basic fibroblast growth
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 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC with its receptor and heparin. These oligonucleotides may inhibit
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 16; Length 4;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
 Db 1 c 1

Search completed: August 24, 2002, 22:08:16
 Job time: 8849 sec

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OM nucleic - nucleic search, using sw mode..

Run on: August 24, 2002, 15:57:42 ; Search time 159.68 Seconds
(without alignments)
30.766 Million cell updates/sec

Title: US-10-077-383-9
Perfect score: 20
Sequence: 1 nnnnnnnnnnnnnnnnnnn 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	0	0.0	1	5	PCT-US93-00977-702
3	0	0.0	2	1	US-08-268-679B-8
4	0	0.0	2	1	US-08-268-679B-8
5	0	0.0	2	1	US-08-457-274A-16
6	0	0.0	2	1	US-08-457-274A-16
7	0	0.0	2	1	US-08-484-192-16
8	0	0.0	2	1	US-08-484-192-16
9	0	0.0	2	2	US-08-726-464B-28
10	0	0.0	2	2	US-08-726-464B-28
11	0	0.0	2	3	US-09-016-520-35
12	0	0.0	2	3	US-09-016-520-35
13	0	0.0	2	4	US-09-130-973-35
14	0	0.0	2	4	US-09-130-973-35
15	0	0.0	2	4	US-09-477-902-35
16	0	0.0	2	4	US-09-477-902-35
17	0	0.0	2	4	US-08-361-024-3
18	0	0.0	2	4	US-08-361-024-3
19	0	0.0	2	4	US-09-411-862A-15
20	0	0.0	2	4	US-09-411-862A-15
21	0	0.0	2	4	US-09-411-862A-16
22	0	0.0	2	4	US-09-411-862A-16
23	0	0.0	2	5	PCT-US95-C5758-16
24	0	0.0	2	5	PCT-US95-C5758-16
25	0	0.0	3	1	US-07-791-213D-46
26	0	0.0	3	1	US-07-791-213D-46
27	0	0.0	3	1	US-07-791-213D-62

Sequence 62, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 36, Appl

ALIGNMENTS

RESULT 1
PCT-US93-00977-702
Sequence 702, Application PC/TUS9300977
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 711
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00977
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 702:
SEQUENCE CHARACTERISTICS:
LENGTH: 1
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-00977-702

Query Match 0.08; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1

Db 1 A 1

RESULT 2
PCT-US93-00977-702/c
; Sequence 702, Application PC/TUS9300977
; GENERAL INFORMATION:
; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
; NUMBER OF SEQUENCES: 711
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson, and Bear
; STREET: 620 Newport Center Dr., Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00977
; FILING DATE: 19930129
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: HITACHI.006H
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 702:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-00977-702

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n l
Db 1 T 1

RESULT 3
US-08-268-679B-8
; Sequence 8, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD; MOLLA,
; APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/268, 679B
; FILING DATE: 30-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07\846, 914
; FILING DATE: 06-MAR-1992
; CLASSIFICATION: 435
; APPLICATION NUMBER: 07\719, 761
; FILING DATE: 24-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MARIA C.H. LIN
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 0887-4095 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: OLIGONUCLEOTIDE
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE: N.A.
; POSITION IN GENOME: N.A.
US-08-268-679B-8

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n l
Db 1 G 1

RESULT 4
US-08-268-679B-8/c
; Sequence 8, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD; MOLLA,
; APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268, 679B
; FILING DATE: 30-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07\846, 914
; FILING DATE: 06-MAR-1992
; CLASSIFICATION: 435
; APPLICATION NUMBER: 07\719, 761
; FILING DATE: 24-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MARIA C.H. LIN

REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 0887-4095 JS2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE: N.A.
POSITION IN GENOME: N.A.
US-08-268-679B-8

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 2 C 2

RESULT 5
US-08-457-274A-16
Sequence 16, Application US/08457274A
Patent No. 5734086
GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
APPLICANT: Tomita, Takashi
TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Musca domestica

STRAIN: Learn-PyR
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 1
US-08-457-274A-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 A 1

RESULT 6
US-08-457-274A-16/c
Sequence 16, Application US/08457274A
Patent No. 5734086
GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
APPLICANT: Tomita, Takashi
TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Musca domestica
STRAIN: Learn-PyR
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 1
US-08-457-274A-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 2 T 2

RESULT 7
US-08-484-192-16
; Sequence 16, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1, "")
; OTHER INFORMATION: /note= "This is a biotin-17
; nucleotide stretch of abasic residues."
US-08-484-192-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 n 1
DB 1 N 1
RESULT 8
US-08-484-192-16/c
; Sequence 16, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN

; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1, "")
; OTHER INFORMATION: /note= "This is a biotin-17
; nucleotide stretch of abasic residues."
US-08-484-192-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
DB 2 C 2

RESULT 9
US-08-726-464B-28
; Sequence 28, Application US/08726464B
; Patent No. 5932546
; GENERAL INFORMATION:
; APPLICANT: BARRETT, Ronald W.
; APPLICANT: DOWER, William J.
; APPLICANT: CWIRLA, Steven A.
; APPLICANT: JOHNSON, Sherril S.
; APPLICANT: WRIGHION, Nicholas C.
; APPLICANT: DUFFIN, David J.
; APPLICANT: WAGSTROM, Christopher R.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO THE
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,464B
FILING DATE: 04-OCT-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-024100
TELEPHONE: 415/576-0200
TELEFAX: 415/576-0300
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
US-08-726-464B-28

Query Match 0.0%; Score 0; DB 2; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 n 1
Db 1 v 1

RESULT 10
US-08-726-464B-28/C
; Sequence 28, Application US/08726464B
; Patent No. 5932546
; GENERAL INFORMATION:
; APPLICANT: BARRETT, Ronald W.
; APPLICANT: DOWER, William J.
; APPLICANT: CWIRLA, Steven A.
; APPLICANT: JOHNSON, Sherril S.
; APPLICANT: WRIGHTON, Nicholas C.
; APPLICANT: DUFFIN, David J.
; APPLICANT: WAGSTROM, Christopher R.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO THE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,464B
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-024100
TELEPHONE: 415/576-0200
TELEFAX: 415/576-0300
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
US-08-726-464B-28

Query Match 0.0%; Score 0; DB 2; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 n 1
Db 2 y 2

RESULT 11
US-09-016-520-35
; Sequence 35, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; EARLIER FILING DATE: 1998-01-30
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-35

Query Match 0.0%; Score 0; DB 3; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 n 1
Db 1 t 1

RESULT 12
US-09-016-520-35/C
; Sequence 35, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides

; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; EARLIER FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
US-09-016-520-35

Query Match 0.0%; Score 0; DB 3; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 2 A 2

RESULT 13
US-09-130-973-35
; Sequence 35, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-dimethylaminooxyethyl thymidine (T'-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-35

Query Match 0.0%; Score 0; DB 4; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 t 1

RESULT 14
US-09-130-973-35/c
; Sequence 35, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:

; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-dimethylaminooxyethyl thymidine (T'-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-35

Query Match 0.0%; Score 0; DB 4; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 2 A 2

RESULT 15
US-09-477-902-35
; Sequence 35, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
US-09-477-902-35

Query Match 0.0%; Score 0; DB 4; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 t 1

Mon Aug 26 10:18:26 2002

us-10-077-383-9.rni

Page 7

Search completed: August 24, 2002, 21:57:39
Job time: 21597 sec


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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 C 1

RESULT 2
HSM001740/c
ID HSM001740 standard; RNA; EST; 1 BP.
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AC AL037411;
XX
SV AL037411.1
XX
12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKF2p564L2071_s1 (from clone DKF2p564L2071)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-1
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No r1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 G 1

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SV AL037411.1
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12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
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DE Homo sapiens mRNA; EST DKF2p564L2071_s1 (from clone DKF2p564L2071)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-1
RA Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by GBF within the cDNA
CC sequencing consortium of the German Genome Project
CC No r1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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FH Key Location/Qualifiers
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FT xl-2blue; sites Noti + Sali"
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FT /tissue_type="brain"
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SQ Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 G 1

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AC AL039393;
XX
SV AL039393.1
XX
12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
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DE Homo sapiens mRNA; EST DKF2p434J0410_s1 (from clone DKF2p434J0410)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

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XX	[1]
RN	1-1
RP	Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RA	; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL	MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XL	
CC	Clone from S. Wiemann, sequenced by Olagen within the cDNA
CC	sequencing consortium of the German Genome Project
CC	this sequence also available at the RZPD in Berlin
CC	This clone is available at the RZPD in Berlin
CC	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC	Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX	Key Location/Qualifiers
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FF	1..1
FT	/db_xref="taxon:9606"
FT	/organism="Homo sapiens"
FT	/clone="DKFZp434J0410"
FT	/clone_lib="434 (synonym: htes3). Vector pSport1; host
FT	DH10B; sites NotI + SalI"
FT	/dev_stage="adult"
FT	/tissue_type="testis"
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SQ	Sequence 1 BP; 1 A; 0 C; 0 G; 0 T; 0 other;
Query Match 0.0%; Score 0; DB 2; Length 1;	
Best Local Similarity 0.0%; Pred. No. 0;	
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 n 1
Db	1 T 1
RESULT	5
ID	HSM005008
AC	HSW005008 standard; RNA; EST; 1 BP.
XC	AL040532;
SV	AL040532.1
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DT	12-MAR-1999 (Rel. 59, Created)
DD	12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE	Homo sapiens mRNA; EST DKFZp434H2214_r1 (from clone DKFZp434H2214)
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KW	EST; expressed sequence tag.
OS	Homo sapiens (human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX	
LN	[1]
RN	1-1
RP	Koehler K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RA	; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL	MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XL	
CC	Clone from S. Wiemann, sequenced by BPFZ within the cDNA
CC	sequencing consortium of the German Genome Project
CC	No sl sequence available
CC	This clone is available at the RZPD in Berlin
CC	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC	Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX	
Key	Location/Qualifiers
FH	

FT	source	1..1
FT	/db_xref=taxon:9606"	
FT	/organism="Homo sapiens"	
FT	/clone="DKFzp434H214"	
FT	/clone_lib="434 (synonym: htes3). Vector pSport1, host	
FT	DH10B; sites NotI + SalI"	
FT	/dev_stage="adult"	
FT	/tissue_type="testis"	
XX		
SQ	Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;	
	Query Match	0.0%; Score 0; DB 2; Length 1;
	Best Local Similarity	0.0%; Pred. No. 0;
	Matches	0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 n 1	
Db	1 C 1	
RESULT	6	
ID	HSW005008/c	
DD	HSW005008 standard; RNA; EST; 1 BP.	
AC	AL040532;	
SV	AL040532.1	
DT	12-MAR-1999 (Rel. 59, Created)	
DT	12-MAR-1999 (Rel. 59, Last updated, Version 1)	
DE	Homo sapiens mRNA; EST DKFzp434H2214_r1 (from clone DKFzp434H2214)	
KW	EST; expressed sequence tag.	
OS	Homo sapiens (human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia	
NC	Eutheria; Primates; Catarrhini; Hominidae; Homo.	
RN	[1]	
RP	1-1	
RA	Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;	
RL	Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.	
RL	MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY	
CC	Clone from S. Wiemann, sequenced by BMFZ within the cDNA	
CC	sequencing consortium of the German Genome Project	
CC	No sl sequence available	
CC	This clone is available at the RZPD in Berlin	
CC	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059	
CC	Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de	
XX		
Key	Location/Qualifiers	
FH		
FT	source	1..1
FT	/db_xref=taxon:9606"	
FT	/organism="Homo sapiens"	
FT	/clone="DKFzp434H2214"	
FT	/clone_lib="434 (synonym: htes3). Vector pSport1; host	
FT	DH10B; sites NotI + SalI"	
FT	/dev_stage="adult"	
FT	/tissue_type="testis"	
XX		
SQ	Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;	
	Query Match	0.0%; Score 0; DB 2; Length 1;
	Best Local Similarity	0.0%; Pred. No. 0;
	Matches	0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 n 1	

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Db      1 G 1

RESULT 7
ID      HSM011115 standard; RNA; EST; 1 BP.
XX
AC      AL046265;
XX
SV      AL046265.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434G017_r1 (from clone DKFZp434G017)
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-1
RA      Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT      ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key      Location/Qualifiers
FT      source      1. .1
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 n 1
DB      1 G 1

RESULT 9
ID      HSM011270 standard; RNA; EST; 1 BP.
XX
AC      AL046420;
XX
SV      AL046420.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434N037_r1 (from clone DKFZp434N037)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-1
RA      Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT      ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
XX
FH      Key      Location/Qualifiers
FT      source      1. .1
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 n 1
DB      1 C 1

RESULT 8
ID      HSM011115/c standard; RNA; EST; 1 BP.
XX
AC      AL046265;
XX
SV      AL046265.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434G017_r1 (from clone DKFZp434G017)
XX

```

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers
 FH source 1. .1
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434N037"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 C 1

RESULT 10
 HSM011270/c
 ID HSM011270 standard; RNA; EST; 1 BP.
 XX
 AC AL046420;
 SV AL046420.1
 DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp434N037_r1 (from clone DKFZp434N037)
 XX
 KW EST; expressed sequence tag.

OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]
 RN Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY

XX Cloned from S. Wiemann, sequenced by BMFZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No SI sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers
 FH source 1. .1
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434N037"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX

SQ Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 G 1

RESULT 11
 HSM011922
 ID HSM011922 standard; RNA; EST; 1 BP.

XX AC AL047072;
 XX SV AL047072.1

DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp586P0817_r1 (from clone DKFZp586P0817)
 XX
 KW EST; expressed sequence tag.

OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]
 RN Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
 XX Cloned from S. Wiemann, sequenced by BMFZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No SI sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers
 FH source 1. .1
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp586P0817"
 FT /clone_lib="586 (synonym: hutel). Vector pSport1; host
 FT DH10B; sites NotI + SalI/MluI"
 FT /dev_stage="adult"
 FT /tissue_type="uterus"
 XX

SQ Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 C 1

RESULT 12
 HSM011922/c
 ID HSM011922 standard; RNA; EST; 1 BP.

XX AC AL047072;
 XX SV AL047072.1

DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA; EST DKFZp586P0817_r1 (from clone DKFZp586P0817)
 XX EST; expressed sequence tag.
 KW Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX [1]
 RN 1-1
 RP Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
 XX Clone from S. Wiemann, sequenced by BMFZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No sl sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de
 XX Key Location/Qualifiers
 FH 1 . 1
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp586P0817"
 FT /clone_lib="586 (synonym: hutel). Vector pSport1; host
 FT DH10B; sites NotI + SalI/MluI"
 FT /dev_stage="adult"
 FT /tissue_type="uterus"
 XX Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 G 1

RESULT 13
 BI416880 1 bp mRNA linear EST 15-AUG-2001
 LOCUS hasp002xj20f Heterobasidion annosum - Scots pine infection stage
 DEFINITION subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
 annosum cDNA clone hasp002xj20f, mRNA sequence.
 ACCESSION BI416880
 VERSION BI416880.1 GI:15187903
 KEYWORDS EST.
 SOURCE Pinus sylvestris/Heterobasidion annosum.
 ORGANISM Pinus sylvestris/Heterobasidion annosum
 Eukaryota; mixed EST libraries.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
 TITLE Expressed sequence tags of randomly selected cDNA clones from the
 interaction of the root rot fungus (Heterobasidion annosum) with
 seedling roots of Scots pine (Pinus sylvestris)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Fred O. Asiegbu
 Dept. of Forest Mycology & Pathology
 Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,
 Sweden
 Tel: +46 18 67 15 98
 Fax: +46 18 30 92 45
 Email: Fred.Asiegbu@mykopat.slu.se
 Seq primer: T7 primer.
 Location/Qualifiers
 1 . 1
 /organism="Pinus sylvestris/Heterobasidion annosum"
 /db_xref="taxon:169015"
 /clone="hasp002xj20f"
 /clone_lib="Heterobasidion annosum - Scots pine infection
 stage subtraction cDNA library (hasp)"
 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
 hybridization cDNA library was constructed from scots
 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (FP5)."
 BASE COUNT 0 a 0 c 0 g 0 t 1 others
 ORIGIN

Query Match 0.0%; Score 0; DB 10; Length 1;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 N 1

RESULT 14
 BI416880/c
 LOCUS hasp002xj20f Heterobasidion annosum - Scots pine infection stage
 DEFINITION subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
 annosum cDNA clone hasp002xj20f, mRNA sequence.
 ACCESSION BI416880
 VERSION BI416880.1 GI:15187903
 KEYWORDS EST.
 SOURCE Pinus sylvestris/Heterobasidion annosum.
 ORGANISM Pinus sylvestris/Heterobasidion annosum
 Eukaryota; mixed EST libraries.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
 TITLE Expressed sequence tags of randomly selected cDNA clones from the
 interaction of the root rot fungus (Heterobasidion annosum) with
 seedling roots of Scots pine (Pinus sylvestris)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Fred O. Asiegbu
 Dept. of Forest Mycology & Pathology
 Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,
 Sweden
 Tel: +46 18 67 15 98
 Fax: +46 18 30 92 45
 Email: Fred.Asiegbu@mykopat.slu.se
 Seq primer: T7 primer.
 Location/Qualifiers
 1 . 1
 /organism="Pinus sylvestris/Heterobasidion annosum"
 /db_xref="taxon:169015"
 /clone="hasp002xj20f"
 /clone_lib="Heterobasidion annosum - Scots pine infection
 stage subtraction cDNA library (hasp)"
 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
 hybridization cDNA library was constructed from scots
 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (FP5)."
 BASE COUNT 0 a 0 c 0 g 0 t 1 others
 ORIGIN

Qy 1 n 1
Db 1 n 1

RESULT 15

BI817896
LOCUS G3-023 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
to putative heterochromatin-like protein 1, mRNA sequence.

ACCESSION BI817896
VERSION BI817896.1 GI:15951508

KEYWORDS

EST.

SOURCE

ORGANISM Ambystoma mexicanum
axolotl.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.

REFERENCE

1 (bases 1 to 1)
Voss,S.R., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,
Gardiner,D.M. and Parichy,D.M.

AUTHORS

Expressed sequence tags from an axolotl limb regeneration library

TITLE

Unpublished (2001)

JOURNAL

Contact: Voss SR

COMMENT

Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel: 970 491 4869
Fax: 970 491 0649
Email: srvoss@amar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate = 5%). Trace file available:
srvoss@amar.colostate.edu.

FEATURES

Location/Qualifiers

1..1
/organism="Ambystoma mexicanum"
/db_xref="taxon:8296"
/clone_lib="Axolotl Lambda Zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

BASE COUNT 0 a 1 c 0 g 0 t

ORIGIN

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. NO. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 c 1

Search completed: August 24, 2002, 21:19:23
Job time: 20525 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: August 24, 2002, 21:54:43 ; Search time 2108.3 Seconds
(without alignments)
198.516 Million cell updates/sec

Title: US-10-077-383-29
Perfect score: 20

Sequence: 1 agagagagagagagagagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description

1	20	100.0	20	6	AR084583	AR084583 Sequence
2	20	100.0	20	6	AR084604	AR084604 Sequence
3	20	100.0	21	6	A64735	A64735 Sequence 1
4	20	100.0	21	6	A64736	A64736 Sequence 2
5	20	100.0	21	6	A64738	A64738 Sequence 4
6	20	100.0	21	6	A64739	A64739 Sequence 5
7	20	100.0	22	6	A64739	A64739 Sequence 5
8	20	100.0	22	6	AX104716	AX104716 Sequence
9	20	100.0	24	6	AR026545	AR026545 Sequence
10	20	100.0	24	6	AR026547	AR026547 Sequence
11	20	100.0	24	6	AR026546	AR026546 Sequence
12	20	100.0	24	6	AR026548	AR026548 Sequence
13	20	100.0	24	6	AR128993	AR128993 Sequence
14	20	100.0	24	6	AR128994	AR128994 Sequence
15	20	100.0	24	6	AR128995	AR128995 Sequence
16	20	100.0	24	6	AR128996	AR128996 Sequence
17	20	100.0	26	6	AS1713	AS1713 Sequence 19
18	20	100.0	26	6	AR167592	AR167592 Sequence
19	20	100.0	26	6	AX323384	AX323384 Sequence
20	20	100.0	26	6	E28852	E28852 Process for
21	20	100.0	27	6	AX175242	AX175242 Sequence
22	20	100.0	28	6	AR142456	AR142456 Sequence
23	20	100.0	32	6	AR002289	AR002289 Sequence
24	20	100.0	32	6	AR053140	AR053140 Sequence
25	20	100.0	38	6	AX207477	AX207477 Sequence
26	20	100.0	41	6	E13926	E13926 Primer. 6/1
27	20	100.0	41	6	E16035	E16035 DNA primer
28	20	100.0	44	6	I31473	I31473 Sequence 38
29	20	100.0	46	6	I22397	I22397 Sequence 5
30	20	100.0	47	6	E13925	E13925 Primer. 6/1
31	20	100.0	47	6	E16034	E16034 DNA primer
32	20	100.0	50	6	AX323400	AX323400 Sequence
33	20	100.0	51	6	AX115977	AX115977 Sequence
34	20	100.0	51	6	AX157871	AX157871 Sequence
35	20	100.0	52	6	AR122336	AR122336 Sequence
36	20	100.0	52	6	I31506	I31506 Sequence 41
37	20	100.0	53	8	CWY17100	Y17100 Cladobotryu
38	20	100.0	55	8	CWY17102	Y17102 Cladobotryu
39	20	100.0	56	8	AF062765	AF062765 Glycine m
40	20	100.0	57	6	AR122341	AR122341 Sequence
41	20	100.0	58	6	AS1707	AS1707 Sequence 13
42	20	100.0	58	6	AS1708	AS1708 Sequence 14
43	20	100.0	58	6	AR167586	AR167586 Sequence
44	20	100.0	58	6	AR167587	AR167587 Sequence
45	20	100.0	58	6	AX323378	AX323378 Sequence
					AX323379	AX323379 Sequence

ALIGNMENTS

RESULT	1	AR084583	Sequence 72 from patent US 5981185.	20 bp	DNA	linear	PAT 01-SEP-2000
LOCUS	AR084583	Sequence 72 from patent US 5981185.					
DEFINITION	AR084583	Sequence 72 from patent US 5981185.					
ACCESSION	AR084583	Sequence 72 from patent US 5981185.					
VERSION	AR084583.1	GI:10011354					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 20)						
AUTHORS	Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.						
TITLE	Oligonucleotide repeat arrays						
JOURNAL	Patent: US 5981185-A 72 09-NOV-1999;						
FEATURES	Location/Qualifiers						
source	1..20						
BASE COUNT	10 a 0 c 10 g 0 t						
ORIGIN	/organism="unknown"						

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 59;

LOCUS A64736 21 bp
DEFINITION Sequence 2 from Patent WO9729116.

BASE COUNT 0 a 12 c 0 g 12 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 20
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Db 23 AGAGAGAGAGAGAGAG 4

RESULT 15

ARI28996
LOCUS 24 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6183966.

ACCESSION ARI28996
VERSION ARI28996.1 GI:14116658

KEYWORDS
SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)

AUTHORS Gray, D.M. and Clark, C.L.

TITLE Apparatus and method for selectively ranking sequences for antisense targeting

JOURNAL Patent: US 6183966-A 11 06-FEB-2001;

FEATURES Location/Qualifiers

source 1..24

/organism="unknown"

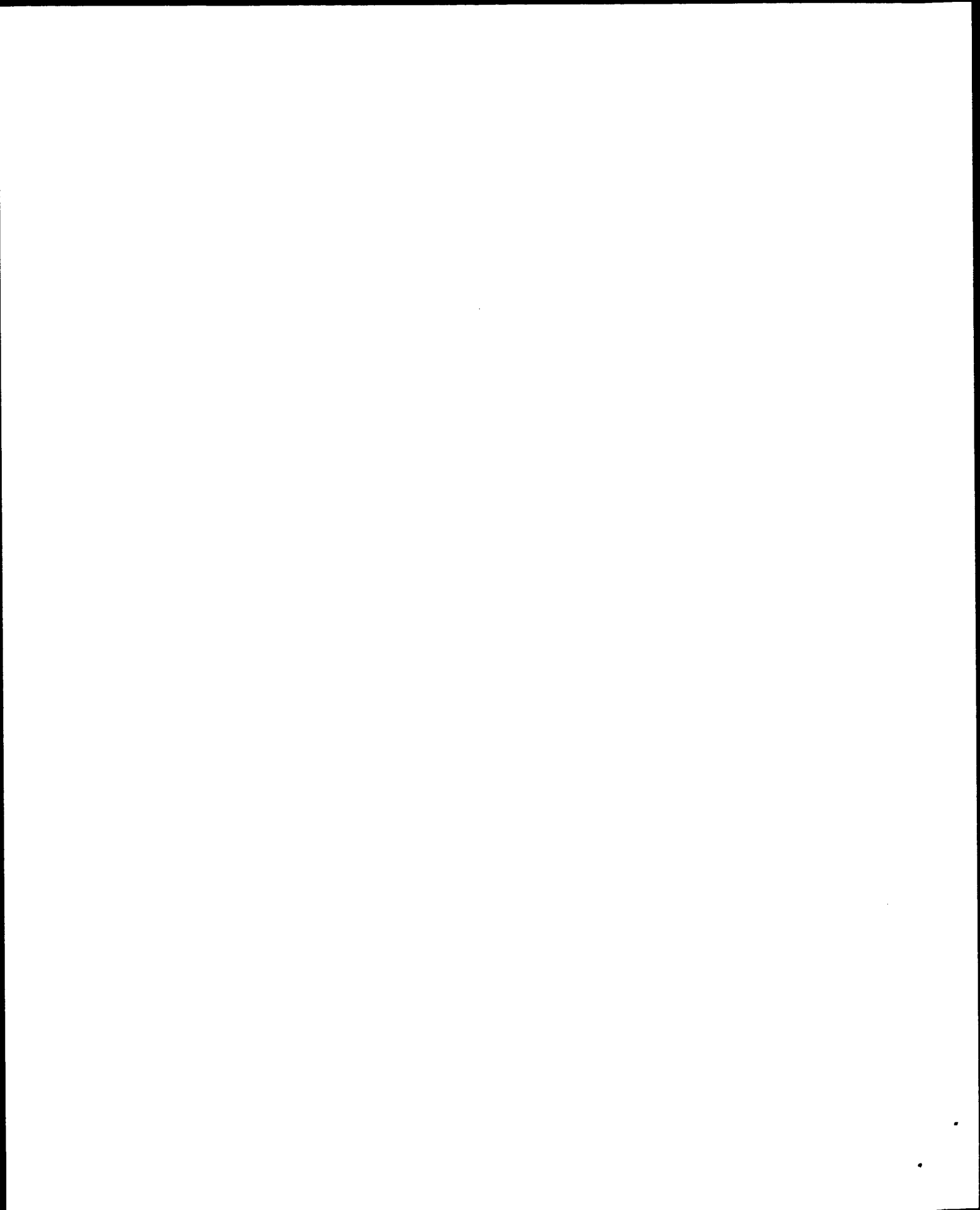
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Best Local Similarity 100.0%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 20
|||||
Db 2 AGAGAGAGAGAGAGAG 21

Search completed: August 24, 2002, 21:54:45
Job time: 22408 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 22:08:16 ; Search time 623.77 Seconds
(without alignments)
55.050 Million cell updates/sec

Title: US-10-077-383-29

Perfect score: 20

Sequence: 1 agagagagagagagagag 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	20	100.0	21	18	AAT86583
C 3	20	100.0	22	13	AAQ33557
C 4	20	100.0	22	22	AAF99703
C 5	20	100.0	23	13	AAQ33511
C 6	20	100.0	24	20	AAQ00524
C 7	20	100.0	24	20	AAQ00526
C 8	20	100.0	24	20	AAQ00525
C 9	20	100.0	24	20	AAQ00527

C 10	20	100.0	24	22	AAF57996	Nucleic acid tripl
C 11	20	100.0	24	22	AAF57997	Nucleic acid tripl
C 12	20	100.0	24	22	AAF57998	Nucleic acid tripl
C 13	20	100.0	24	22	AAF57999	Nucleic acid tripl
C 14	20	100.0	24	22	AAF58000	Nucleic acid tripl
C 15	20	100.0	24	22	AAF58001	Nucleic acid tripl
C 16	20	100.0	24	22	AAF58002	Nucleic acid tripl
C 17	20	100.0	24	22	AAF58003	Nucleic acid tripl
C 18	20	100.0	24	22	AAF58004	Nucleic acid tripl
C 19	20	100.0	24	22	AAF58005	Nucleic acid tripl
C 20	20	100.0	24	22	AAF58006	Nucleic acid tripl
C 21	20	100.0	24	22	AAF58007	Nucleic acid tripl
C 22	20	100.0	24	22	AAF58008	Nucleic acid tripl
C 23	20	100.0	24	22	AAF58009	Nucleic acid tripl
C 24	20	100.0	24	22	AAF58010	Nucleic acid tripl
C 25	20	100.0	24	22	AAF58011	Nucleic acid tripl
C 26	20	100.0	24	22	AAF58012	Nucleic acid tripl
C 27	20	100.0	24	22	AAF58013	Nucleic acid tripl
C 28	20	100.0	24	22	AAF58014	Nucleic acid tripl
C 29	20	100.0	24	22	AAF58015	Nucleic acid tripl
C 30	20	100.0	24	22	AAF58016	Nucleic acid tripl
C 31	20	100.0	24	22	AAF58017	Nucleic acid tripl
C 32	20	100.0	24	22	AAF58018	Nucleic acid tripl
C 33	20	100.0	24	22	AAF58019	Nucleic acid tripl
C 34	20	100.0	24	22	AAF58020	Nucleic acid tripl
C 35	20	100.0	24	22	AAF58021	Nucleic acid tripl
C 36	20	100.0	24	22	AAF58022	Nucleic acid tripl
C 37	20	100.0	24	22	AAF58023	Nucleic acid tripl
C 38	20	100.0	24	22	AAF58024	Nucleic acid tripl
C 39	20	100.0	24	22	AAF58025	Nucleic acid tripl
C 40	20	100.0	24	22	AAF58026	Nucleic acid tripl
C 41	20	100.0	24	22	AAF58027	Nucleic acid tripl
C 42	20	100.0	24	22	AAF58028	Nucleic acid tripl
C 43	20	100.0	24	22	AAF58029	Nucleic acid tripl
C 44	20	100.0	24	22	AAF58030	Nucleic acid tripl
C 45	20	100.0	24	22	AAF58031	Nucleic acid tripl

ALIGNMENTS

RESULT 1	
AAT86582/c	
ID	AAT86582 standard; DNA; 21 BP.
XX	
AC	AAT86582;
XX	
XX	25-MAR-1998 (first entry)
DT	
DE	Phosphorothioate oligonucleotide #1.
XX	
XX	Phosphorothioate oligonucleotide; dimeric phosphoramidite syntho;
KW	thioester; DNA synthesis; antisense oligonucleotide; gene therapy;
XX	ss.
XX	
OS	Synthetic.
XX	
EH	Key
FT	Location/Qualifiers
FT	misc_difference 1..21
FT	/*tag= a
FT	/note= "Phosphorothioate linkages between alternate
FT	nucleotides (1 and 2, 3 and 4 etc.)"
XX	
PN	WO9729116-A1.
XX	
PD	14-AUG-1997.
XX	
PF	06-FEB-1997; 97WO-GB00327.
XX	
PR	06-FEB-1996; 96GB-0002326.
XX	
PA	(CRUA-) CRUACHEM LTD.
XX	

PI Rao MV, Reese CB;
 XX WPI; 1997-415290/38.
 XX Solid phase synthesis of phosphorothioate oligonucleotide(s) using
 PT new dimeric synthon(s) - useful as anti:sense molecules for
 PT inhibiting gene expression
 XX Example 3; Page 20; 38pp; English.
 XX The present sequence represents a phosphorothioate oligonucleotide which
 CC was prepared by solid phase synthesis. The method comprises adding at
 CC least one dimeric phosphoramidite synthon, optionally having a protected
 CC thioester group in its internucleotide link, during the synthesis cycle.
 CC These novel dimeric phosphoramidite synthons are used as antisense
 CC molecules for inhibition of gene expression. The method gives increased
 CC yields of the phosphorothioate oligonucleotide (since fewer cycles are
 CC needed) and facilitates separation of impurities (greater difference
 CC in size compared with use of monomeric synthons).
 XX Sequence 21 BP; 0 A; 10 C; 10 G; 11 T; 0 other;
 SQ

Query Match 100.0%; Score 20; DB 18; Length 21;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
 |||||
 DB 21 AGAGAGAGAGAGAGAGAG 2

RESULT 2
 AAT86583/c
 ID AAT86583 standard; DNA; 21 BP.
 XX
 AC AAT86583;
 XX
 DT 25-MAR-1998 (first entry)
 XX
 DE Phosphorothioate oligonucleotide #2.
 XX
 KW Phosphorothioate oligonucleotide; dimeric phosphoramidite synthon;
 KW thioester; DNA synthesis; antisense oligonucleotide; gene therapy;
 KW ss.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH misc_difference 1..21
 FT /*tag= a
 FT /note= "Phosphorothioate linkages between alternate
 FT nucleotides (1 and 2, 3 and 4 etc.)"
 XX
 PN WO9729116-A1.
 XX
 PD 14-AUG-1997.
 XX
 PP 06-FEB-1997; 97WO-GB00327.
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 PR 06-FEB-1996; 96GB-0002326.
 XX
 PA (CRUA-) CRUACHEM LTD.
 XX
 PI Rao MV, Reese CB;
 XX
 DR WPI; 1997-415290/38.
 XX
 PT Solid phase synthesis of phosphorothioate oligo:nucleotide(s) using
 PT new dimeric synthon(s) - useful as anti:sense molecules for
 PT inhibiting gene expression
 XX Example 3; Page 25; 38pp; English.

XX The present sequence represents a phosphorothioate oligonucleotide which
 CC was prepared by solid phase synthesis. The method comprises adding at
 CC least one dimeric phosphoramidite synthon, optionally having a protected
 CC thioester group in its internucleotide link, during the synthesis cycle.
 CC These novel dimeric phosphoramidite synthons are used as antisense
 CC molecules for inhibition of gene expression. The method gives increased
 CC yields of the phosphorothioate oligonucleotide (since fewer cycles are
 CC needed) and facilitates separation of impurities (greater difference
 CC in size compared with use of monomeric synthons).
 XX Sequence 21 BP; 1 A; 10 C; 0 G; 10 T; 0 other;
 SQ

Query Match 100.0%; Score 20; DB 18; Length 21;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
 |||||
 DB 20 AGAGAGAGAGAGAGAGAG 1

RESULT 3
 AAQ33557
 ID AAQ33557 standard; DNA; 22 BP.
 XX
 AC AAQ33557;
 XX
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone AGLA248.
 XX
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 OS
 PN WO9213102-A.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US00340.
 XX
 PR 15-JAN-1991; 91US-0642342.
 XX
 PA (GENM-) GENMARK.
 XX
 PI Georges M, Massey JM;
 DR WPI; 1992-284684/34.
 XX
 PT Polymorphic bovine DNA markers - used in genetic identification,
 PT gene mapping, and selective breeding
 XX
 PS Table 7; Page 151; 517pp; English.
 XX
 CC The sequence is that of a bovine microsatellite sequence obt'd. by
 CC screening a library of bovine MboI DNA fragments of between
 CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
 CC One out of 50 clones cross-hybridised. Assuming independent
 CC distribution of microsatellites and MboI sites, the frequency of
 CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
 CC 000. The sequence information for ca. 230 such bovine microsatellites
 CC is summarised in the specification and indexed herein (see below).
 CC The sequences upstream and downstream of the microsatellite sequence
 CC were used to generate the required PCR primers for in vitro
 CC amplification of the corresp. microsatellite (using the program
 CC OPTIPRIM). The microsatellites may be used to identify individuals,
 CC for parentage testing, and in the genetic mapping of economic trait
 CC loci, or genes involved in the determination of economically important
 CC traits esp. in cattle, to allow selective breeding.
 CC See also AAQ33501-34437.

XX
SQ Sequence 22 BP; 11 A; 0 C; 10 G; 0 U; 1 other;

Query Match 100.0%; Score 20; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agagagagagagagagagag 20
|||||
Db 3 agagagagagagagagagag 22
|||||

RESULT 4
AAF99703/C
ID AAF99703 standard; DNA; 22 BP.

XX AAF99703;

XX 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #819.

XX Vaccines; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW Immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

XX Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US26383.

XX 25-SEP-1999; 99US-0156113.

XX 27-SEP-1999; 99US-0156135.

XX 23-AUG-2000; 2000US-0227436.

XX (IOWA) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

XX Vaccinating against tumors, infectious diseases, allergies and asthma
using immunostimulatory Py-rich and TG nucleic acids -

XX CladM 101; Page 56; 338pp; English.

XX The present invention relates to a method for stimulating an immune
response. The method comprises administering an immunostimulatory nucleic
acid to a non-rodent subject in sufficient quantity to stimulate an
immune response. The present sequence is one such immunostimulatory
nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
haemophilus, campylobacter, clostridium, Escherichia coli and/or
staphylococcus), fungal antigens and/or parasitic antigens. The method is
also useful for preventing cancer, asthma, infectious disease, allergy or
immune deficiency. The present sequence can also be used to redirect a
Th2 to a Th1 immune response and to activate immune cells.
XX Note: the present sequence may have a phosphorothioate backbone.

XX Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agagagagagagagagagag 20
|||||
Db 22 AGAGAGAGAGAGAGAGAG 3
|||||

RESULT 5
AAQ33511
ID AAQ33511 standard; DNA; 23 BP.

XX AAQ33511;

XX 02-FEB-1993 (first entry)

XX Sequence of microsatellite from clone AGLA209.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;

XX genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US00340.

XX 15-JAN-1991; 91US-0642342.

XX (GENN-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification,
gene mapping, and selective breeding

XX Table 7; Page 132; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
screening a genomic library of bovine MboI DNA fragments of between
250 and 500 bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe.
XX One out of 50 clones cross-hybridised. Assuming independent
distribution of microsatellites and MboI sites, the frequency of
(T)₆n > 9 microsatellites in the bovine genome is estimated at >100.
XX 000. The sequence information for ca. 230 such bovine microsatellites
is summarised in the specification and indexed herein (see below).
XX The sequences upstream and downstream of the microsatellite sequence
were used to generate the required PCR primers for in vitro
amplification of the corresp. microsatellite (using the program
OPTIPRIM). The microsatellites may be used to identify individuals,
for parentage testing, and in the genetic mapping of economic trait
loci, or genes involved in the determination of economically important
traits esp. in cattle, to allow selective breeding.
XX See also AAQ33501-34437.

XX Sequence 23 BP; 12 A; 0 C; 11 G; 0 U; 0 other;

Query Match 100.0%; Score 20; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agagagagagagagagagag 20
|||||
Db 1 agagagagagagagagagag 20
|||||

RESULT 6
AA00524
ID AAX00524 standard; mRNA; 24 BP.

```

AC AAX00524;
XX
DT 30-MAR-1999 (first entry)
XX
DE Target sequence #2 for antisense oligonucleotides.
XX
KW Target; antisense; selective rank; inhibition; ranking; stability;
KW interaction; ss.
XX
OS Synthetic.
XX
PN US5856103-A.
XX
PD 05-JAN-1999.
XX
PF 03-MAR-1997; 97US-0808474.
XX
PR 03-MAR-1997; 97US-0808474.
PR 07-OCT-1994; 94US-0320507.
XX
PA (TEXA ) UNIV TEXAS.
XX
PI Clark CL, Gray DM;
XX
DR WPI; 1999-105098/09.
XX
XX Selectively ranking nucleic acid molecules, for inhibitory
PT efficiency - comprises determining the fraction a set of
PT nearest-neighbour nucleic acid base pair types in a target sequence
PT zone, substituting nearest-neighbour nucleic acid base pair
PT fractions to determine the fractions and multiplying
XX
PS Disclosure; Column 13-14; 72pp; English.
XX
CC This sequence represents a target mRNA for the generation of antisense
CC oligonucleotides (ASO) in a method of selectively ranking nucleic acid
CC molecules for inhibitory efficiency. The method comprises:
CC (a) determining the fraction of each of a set of 13 nearest-neighbour
CC nucleic acid base pair types in a target sequence zone RNA:ASO-DNA hybrid
CC nucleic acid sequence; (b) substituting nearest-neighbour nucleic acid
CC base pair fractions into formulas to determine the fractions of each of
CC a series of 13 nearest-neighbour nucleic acid base pair types to provide
CC determined fractions; and (c) multiplying the fractions of the 13
CC nearest-neighbour nucleic acid base pair types by a stability ranking
CC to the nucleic acid antisense sequence; where the results are ordered
CC to produce a ranking. The process is used to rank nucleic acid sequences
CC based on the stability of nucleic acid oligomer binding interactions to
CC select sequence zones for antisense targeting.
XX
SQ Sequence 24 BP; 12 A; 0 C; 12 G; 0 U; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
Db 1 agagagagagagagagagag 20

RESULT 7
AAX00526/c
ID AAX00526 standard; mRNA; 24 BP.
XX
AC AAX00526;
XX
DT 30-MAR-1999 (first entry)
XX
DE Poly-pyrimidine target sequence for antisense oligonucleotides.
XX
KW Target; antisense; selective rank; inhibition; ranking; stability;
KW interaction; ss.

```

```

XX
OS Synthetic.
XX
PN US5856103-A.
XX
PD 05-JAN-1999.
XX
PF 03-MAR-1997; 97US-0808474.
XX
PR 03-MAR-1997; 97US-0808474.
PR 07-OCT-1994; 94US-0320507.
XX
PA (TEXA ) UNIV TEXAS.
XX
PI Clark CL, Gray DM;
XX
DR WPI; 1999-105098/09.
XX
XX Selectively ranking nucleic acid molecules, for inhibitory
PT efficiency - comprises determining the fraction a set of
PT nearest-neighbour nucleic acid base pair types in a target sequence
PT zone, substituting nearest-neighbour nucleic acid base pair
PT fractions to determine the fractions and multiplying
XX
PS Disclosure; Column 13-14; 72pp; English.
XX
CC This sequence represents a target mRNA for the generation of antisense
CC oligonucleotides (ASO) in a method of selectively ranking nucleic acid
CC molecules for inhibitory efficiency. The method comprises:
CC (a) determining the fraction of each of a set of 13 nearest-neighbour
CC nucleic acid base pair types in a target sequence zone RNA:ASO-DNA hybrid
CC nucleic acid sequence; (b) substituting nearest-neighbour nucleic acid
CC base pair fractions into formulas to determine the fractions of each of
CC a series of 13 nearest-neighbour nucleic acid base pair types to provide
CC determined fractions; and (c) multiplying the fractions of the 13
CC nearest-neighbour nucleic acid base pair types by a stability ranking
CC to the nucleic acid antisense sequence; where the results are ordered
CC to produce a ranking. The process is used to rank nucleic acid sequences
CC based on the stability of nucleic acid oligomer binding interactions to
CC select sequence zones for antisense targeting.
XX
SQ Sequence 24 BP; 0 A; 12 C; 0 G; 12 U; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
Db 23 AGAGAGAGAGAGAGAGAG 4

RESULT 8
AAX00525/c
ID AAX00525 standard; DNA; 24 BP.
XX
AC AAX00525;
XX
DT 30-MAR-1999 (first entry)
XX
DE Antisense oligonucleotide for poly-purine target sequence.
XX
KW Target; antisense; selective rank; inhibition; ranking; stability;
KW interaction; ss.
XX
OS Synthetic.
XX
PN US5856103-A.
XX
PD 05-JAN-1999.
XX
PF 03-MAR-1997; 97US-0808474.

```

```

XX 03-MAR-1997; 97US-0808474.
PR 07-OCT-1994; 94US-0320507.
XX (TEXA ) UNIV TEXAS.
XX Clark CL, Gray DM;
XX WPI; 1999-105098/09.
XX
XX Selectively ranking nucleic acid molecules, for inhibitory
PT efficiency - comprises determining the fraction a set of
PT nearest-neighbour nucleic acid base pair types in a target sequence
PT zone, substituting nearest-neighbour nucleic acid base pair
PT fractions to determine the fractions and multiplying
XX
PS Disclosure; Column 13-14; 72pp; English.
XX
XX This oligonucleotide represents an antisense oligonucleotides (ASO)
CC targeted to a poly-purine mRNA sequence generated by a method of
CC selectively ranking nucleic acid molecules for inhibitory efficiency.
CC The method comprises: (a) determining the fraction of each of a set of
CC 13 nearest-neighbour nucleic acid base pair types in a target sequence
CC zone RNA:ASO-DNA hybrid nucleic acid sequence; (b) substituting
CC nearest-neighbour nucleic acid base pair fractions into formulas to
CC determine the fractions of each of a series of 13 nearest-neighbour
CC nucleic acid base pair types to provide determined fractions; and
CC (c) multiplying the fractions of the 13 nearest-neighbour nucleic acid
CC base pair types by a stability ranking to the nucleic acid antisense
CC sequence; where the results are ordered to produce a ranking.
CC The process is used to rank nucleic acid sequences based on the
CC stability of nucleic acid oligomer binding interactions to select
CC sequence zones for antisense targeting.
XX
SQ Sequence 24 BP; 0 A; 12 C; 0 G; 12 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
Db 24 AGAGAGAGAGAGAGAGAG 5

RESULT 9
AAX00527
ID AAX00527 standard; DNA; 24 BP.
XX
XX AAX00527;
XX
XX 30-MAR-1999 (first entry)
XX
XX Antisense oligonucleotide for poly-pyrimidine target sequence.
XX
XX Target; antisense; selective rank; inhibition; ranking; stability;
XX interaction; ss.
XX
XX Synthetic.
XX
XX US5856103-A.
XX
XX 05-JAN-1999.
XX
XX 03-MAR-1997; 97US-0808474.
XX
XX 03-MAR-1997; 97US-0808474.
XX 07-OCT-1994; 94US-0320507.
XX
XX (TEXA ) UNIV TEXAS.
XX Clark CL, Gray DM;
XX

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XX WPI; 1999-105098/09.
XX
XX Selectively ranking nucleic acid molecules, for inhibitory
PT efficiency - comprises determining the fraction a set of
PT nearest-neighbour nucleic acid base pair types in a target sequence
PT zone, substituting nearest-neighbour nucleic acid base pair
PT fractions to determine the fractions and multiplying
XX
PS Disclosure; Column 13-14; 72pp; English.
XX
XX This oligonucleotide represents an antisense oligonucleotides (ASO)
CC targeted to a poly-pyrimidine mRNA sequence generated by a method of
CC selectively ranking nucleic acid molecules for inhibitory efficiency.
CC The method comprises: (a) determining the fraction of each of a set of
CC 13 nearest-neighbour nucleic acid base pair types in a target sequence
CC zone RNA:ASO-DNA hybrid nucleic acid sequence; (b) substituting
CC nearest-neighbour nucleic acid base pair fractions into formulas to
CC determine the fractions of each of a series of 13 nearest-neighbour
CC nucleic acid base pair types to provide determined fractions; and
CC (c) multiplying the fractions of the 13 nearest-neighbour nucleic acid
CC base pair types by a stability ranking to the nucleic acid antisense
CC sequence; where the results are ordered to produce a ranking.
CC The process is used to rank nucleic acid sequences based on the
CC stability of nucleic acid oligomer binding interactions to select
CC sequence zones for antisense targeting.
XX
SQ Sequence 24 BP; 12 A; 0 C; 12 G; 0 U; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
Db 2 agagagagagagagagagag 21

RESULT 10
AAF57996/c
ID AAF57996 standard; DNA; 24 BP.
XX
XX AAF57996;
XX
XX 26-APR-2001 (first entry)
XX
XX Nucleic acid triplex DNA sequence #1.
XX
XX Hoogsteen-paired duplex; Watson-Crick pairing; triplex;
XX antisense therapy; gene expression control; transcription; ss.
XX
XX Synthetic.
XX
XX WO200105937-A2.
XX
XX 25-JAN-2001.
XX
XX 20-JUL-2000; 2000WO-US19783.
XX
XX 20-JUL-1999; 99US-0357424.
XX 19-JAN-2000; 2000US-0487130.
XX
XX (TEXA ) UNIV TEXAS.
XX
XX Gray DM, Hashem GM;
XX
XX WPI; 2001-159523/16.
XX
XX Generating nucleic acid molecule comprising Hoogsteen-paired
PT RNAsteriskDNA pyrimidineasteriskpurine duplex for use as an antisense
PT molecule, by heating a triplex to dissociate a Watson-Crick paired
PT pyrimidine strand.

```

XX Example 1; Page 9; 23pp; English.

CC The present invention describes a method for producing a nucleic acid
 CC molecule comprising a Hoogsteen-paired RNA:DNA duplex capable of being
 CC used as an antisense molecule and capable of recognising an RNA sequence
 CC to form a triplex. This involves Watson-Crick pairing. This is useful in
 CC antisense therapy, as it controls gene expression by causing
 CC transcription to be prevented. The present sequence is an example of a
 CC triplex sequence used in the methods of the invention.

XX Sequence 24 BP; 0 A; 12 C; 0 G; 12 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
 |||||
 Db 24 AGAGAGAGAGAGAGAGAG 5

RESULT 11

AAF57997
 ID AAF57997 standard; DNA; 24 BP.

XX AAF57997;

DT 26-APR-2001 (first entry)

DE Nucleic acid triplex DNA sequence #2.

XX Hoogsteen-paired duplex; Watson-Crick pairing; triplex;

KW antisense therapy; gene expression control; transcription; ss.

OS Synthetic.

PN WO200105937-A2.

PD 25-JAN-2001.

XX 20-JUL-2000; 2000WO-US19783.

PR 20-JUL-1999; 99US-0357424.

PR 19-JAN-2000; 2000US-0487130.

PA (TEXA) UNIV TEXAS.

PI Gray DM, Hashem GM;

XX WPI; 2001-159523/16.

XX Generating nucleic acid molecule comprising Hoogsteen-paired

PT RNAsteriskDNA pyrimidinesteriskpurine duplex for use as an antisense

PT molecule, by heating a triplex to dissociate a Watson-Crick paired

PT pyrimidine strand -

XX Example 1; Page 9; 23pp; English.

CC The present invention describes a method for producing a nucleic acid
 CC molecule comprising a Hoogsteen-paired RNA:DNA duplex capable of being
 CC used as an antisense molecule and capable of recognising an RNA sequence
 CC to form a triplex. This involves Watson-Crick pairing. This is useful in
 CC antisense therapy, as it controls gene expression by causing
 CC transcription to be prevented. The present sequence is an example of a
 CC triplex sequence used in the methods of the invention.

XX Sequence 24 BP; 12 A; 0 C; 12 G; 0 U; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 18;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
 |||||
 Db 1 agagagagagagagagagag 20

RESULT 12

AAF57998/C
 ID AAF57998 standard; DNA; 24 BP.

XX AAF57998;

XX 26-APR-2001 (first entry)

DE Nucleic acid triplex DNA sequence #3.

XX Hoogsteen-paired duplex; Watson-Crick pairing; triplex;

KW antisense therapy; gene expression control; transcription; ss.

OS Synthetic.

PN WO200105937-A2.

PD 25-JAN-2001.

XX 20-JUL-2000; 2000WO-US19783.

PR 20-JUL-1999; 99US-0357424.

PR 19-JAN-2000; 2000US-0487130.

PA (TEXA) UNIV TEXAS.

PI Gray DM, Hashem GM;

XX WPI; 2001-159523/16.

XX Generating nucleic acid molecule comprising Hoogsteen-paired
 PT RNAsteriskDNA pyrimidinesteriskpurine duplex for use as an antisense
 PT molecule, by heating a triplex to dissociate a Watson-Crick paired
 PT pyrimidine strand -

XX Example 1; Page 9; 23pp; English.

CC The present invention describes a method for producing a nucleic acid
 CC molecule comprising a Hoogsteen-paired RNA:DNA duplex capable of being
 CC used as an antisense molecule and capable of recognising an RNA sequence
 CC to form a triplex. This involves Watson-Crick pairing. This is useful in
 CC antisense therapy, as it controls gene expression by causing
 CC transcription to be prevented. The present sequence is an example of a
 CC triplex sequence used in the methods of the invention.

XX Sequence 24 BP; 0 A; 12 C; 0 G; 12 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
 |||||
 Db 24 AGAGAGAGAGAGAGAGAG 5

RESULT 13

AAF57999/C
 ID AAF57999 standard; RNA; 24 BP.

XX AAF57999;

XX 26-APR-2001 (first entry)

DE Nucleic acid triplex RNA sequence #1.

```
XX Hoogsteen-paired duplex; Watson-Crick pairing; triplex;  
KW antisense therapy; gene expression control; transcription; ss.  
XX Synthetic.  
OS  
XX WO200105937-A2.  
PN 25-JAN-2001.  
XX  
PF 20-JUL-2000; 2000WO-US19783.  
XX  
PR 20-JUL-1999; 99US-0357424.  
PR 19-JAN-2000; 2000US-0487130.  
XX (TEXA ) UNIV TEXAS.  
PA  
XX Gray DM, Hashem GM;  
XX WPI; 2001-159523/16.  
DR  
XX Generating nucleic acid molecule comprising Hoogsteen-paired  
PT RNAsteriskDNA pyrimidineesteriskpurine duplex for use as an antisense  
PT molecule, by heating a triplex to dissociate a Watson-Crick paired  
PT pyrimidine strand -  
XX Claim 14; Page 17; 23pp; English.  
PS  
XX The present invention describes a method for producing a nucleic acid  
CC molecule comprising a Hoogsteen-paired RNA:DNA duplex capable of being  
CC used as an antisense molecule and capable of recognising an RNA sequence  
CC to form a triplex. This involves Watson-Crick pairing. This is useful in  
CC antisense therapy, as it controls gene expression by causing  
CC transcription to be prevented. The present sequence is an example of a  
CC triplex sequence used in the methods of the invention.  
XX Sequence 24 BP; 0 A; 12 C; 0 G; 12 U; 0 other;  
SQ  
Query Match 100.0%; Score 20; DB 22; Length 24;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 agagagagagagagagagag 20  
Db 24 AGAGAGAGAGAGAGAGAG 5  
RESULT 14  
AAF58000  
ID AAF58000 standard; DNA; 24 BP.  
XX  
AC AAF58000;  
XX  
DT 26-APR-2001 (first entry)  
XX  
DE Nucleic acid triplex DNA sequence #4.  
KW Hoogsteen-paired duplex; Watson-Crick pairing; triplex;  
KW antisense therapy; gene expression control; transcription; ss.  
XX Synthetic.  
OS  
XX WO200105937-A2.  
PN 25-JAN-2001.  
XX  
PF 20-JUL-2000; 2000WO-US19783.  
XX  
PR 20-JUL-1999; 99US-0357424.  
PR 19-JAN-2000; 2000US-0487130.  
XX (TEXA ) UNIV TEXAS.  
PA
```

```
XX Gray DM, Hashem GM;  
XX WPI; 2001-159523/16.  
DR  
XX Generating nucleic acid molecule comprising Hoogsteen-paired  
PT RNAsteriskDNA pyrimidineesteriskpurine duplex for use as an antisense  
PT molecule, by heating a triplex to dissociate a Watson-Crick paired  
PT pyrimidine strand -  
XX Claim 14; Page 17; 23pp; English.  
PS  
XX The present invention describes a method for producing a nucleic acid  
CC molecule comprising a Hoogsteen-paired RNA:DNA duplex capable of being  
CC used as an antisense molecule and capable of recognising an RNA sequence  
CC to form a triplex. This involves Watson-Crick pairing. This is useful in  
CC antisense therapy, as it controls gene expression by causing  
CC transcription to be prevented. The present sequence is an example of a  
CC triplex sequence used in the methods of the invention.  
XX Sequence 24 BP; 12 A; 0 C; 12 G; 0 U; 0 other;  
SQ  
Query Match 100.0%; Score 20; DB 22; Length 24;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 agagagagagagagagagag 20  
Db 1 ageagagagagagagagag 20  
RESULT 15  
AAF58001/C  
ID AAF58001 standard; RNA; 24 BP.  
XX  
AC AAF58001;  
XX  
DT 26-APR-2001 (first entry)  
XX  
DE Nucleic acid triplex RNA sequence #2.  
KW Hoogsteen-paired duplex; Watson-Crick pairing; triplex;  
KW antisense therapy; gene expression control; transcription; ss.  
XX Synthetic.  
OS  
XX WO200105937-A2.  
PN 25-JAN-2001.  
XX  
PF 20-JUL-2000; 2000WO-US19783.  
XX  
PR 20-JUL-1999; 99US-0357424.  
PR 19-JAN-2000; 2000US-0487130.  
XX (TEXA ) UNIV TEXAS.  
PA  
XX Gray DM, Hashem GM;  
XX WPI; 2001-159523/16.  
DR  
XX Generating nucleic acid molecule comprising Hoogsteen-paired  
PT RNAsteriskDNA pyrimidineesteriskpurine duplex for use as an antisense  
PT molecule, by heating a triplex to dissociate a Watson-Crick paired  
PT pyrimidine strand -  
XX Claim 14; Page 17; 23pp; English.  
PS  
XX The present invention describes a method for producing a nucleic acid  
CC molecule comprising a Hoogsteen-paired RNA:DNA duplex capable of being  
CC used as an antisense molecule and capable of recognising an RNA sequence  
CC to form a triplex. This involves Watson-Crick pairing. This is useful in  
CC antisense therapy, as it controls gene expression by causing  
CC transcription to be prevented. The present sequence is an example of a  
CC triplex sequence used in the methods of the invention.  
XX Sequence 24 BP; 12 A; 0 C; 12 G; 0 U; 0 other;  
SQ
```

CC antisense therapy, as it controls gene expression by causing
 CC transcription to be prevented. The present sequence is an example of a
 CC triplex sequence used in the methods of the invention.

XX

SQ Sequence 24 BP; 0 A; 12 C; 0 G; 1 T; 11 U; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20

|||||

Db 24 AGAGAGAGAGAGAGAGAG 5

Search completed: August 24, 2002, 22:08:16
 Job time: 8849 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 21:57:39 ; Search time 159.68 Seconds
(without alignments)
30.766 Million cell updates/sec

Title: US-10-077-383-29

Perfect score: 20

Sequence: 1 agagagagagagagagag 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	20	100.0	20	2	US-08-863-639A-93
3	20	100.0	24	2	US-08-808-474A-8
4	20	100.0	24	2	US-08-808-474A-9
5	20	100.0	24	2	US-08-808-474A-10
6	20	100.0	24	2	US-08-808-474A-11
7	20	100.0	24	4	US-09-235-614-8
8	20	100.0	24	4	US-09-235-614-9
9	20	100.0	24	4	US-09-235-614-10
10	20	100.0	24	4	US-09-235-614-11
11	20	100.0	26	4	US-08-860-038-19
12	20	100.0	26	4	US-09-580-923-19
13	20	100.0	28	3	US-08-946-138-1
14	20	100.0	28	4	US-09-225-652-1
15	20	100.0	32	1	US-08-469-8028-28
16	20	100.0	32	2	US-08-267-8038-46
17	20	100.0	44	1	US-08-222-177A-385
18	20	100.0	46	1	US-08-249-112-5
19	20	100.0	46	5	PCR-US95-06556-5
20	20	100.0	50	4	US-09-580-923-35
21	20	100.0	52	1	US-08-222-177A-418
22	20	100.0	52	4	US-09-224-818A-2
23	20	100.0	57	4	US-09-224-818A-7
24	20	100.0	58	4	US-08-860-038-13
25	20	100.0	58	4	US-08-860-038-14
26	20	100.0	58	4	US-09-580-923-13
27	20	100.0	58	4	US-09-580-923-14

Sequence 244, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 166, Appl
Sequence 430, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 38, Appl
Sequence 30, Appl
Sequence 23, Appl
Sequence 43, Appl
Sequence 9, Appl
Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-863-639A-72
; Sequence 72, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Gaskoy, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863.639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-72

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 agagagagagagagagag 20
|||||

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Db      1  AGAGAGAGAGAGAGAGAG 20

RESULT 2
US-08-863-639A-93/C
; Sequence 93, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-93

Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  agagagagagagagagag 20
        |||
Db      20  AGAGAGAGAGAGAGAGAG 1

RESULT 3
US-08-808-474A-8
; Sequence 8, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776

Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  agagagagagagagagag 20
        |||
Db      20  AGAGAGAGAGAGAGAGAG 1

RESULT 4
US-08-808-474A-9/C
; Sequence 9, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,474A
; FILING DATE: 03-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTDAL:001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 740-8000
; TELEFAX: (214) 740-8800
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-808-474A-9
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Query Match 100.0%; Score 20; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||
DB 23 AGAGAGAGAGAGAGAGAG 4

RESULT 5

US-08-808-474A-10/c
; Sequence 10, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; TITLE OF INVENTION: FOR ANTISENSE TARGETING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,474A
; FILING DATE: 03-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTDAL:001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 740-8000
; TELEFAX: (214) 740-8800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-808-474A-10

Query Match 100.0%; Score 20; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||
DB 23 AGAGAGAGAGAGAGAGAG 4

RESULT 6

US-08-808-474A-11
; Sequence 11, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; TITLE OF INVENTION: FOR ANTISENSE TARGETING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200

; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,474A
; FILING DATE: 03-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTDAL:001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 740-8000
; TELEFAX: (214) 740-8800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-808-474A-11

Query Match 100.0%; Score 20; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||
DB 1 AGAGAGAGAGAGAGAGAG 20

RESULT 7

US-09-235-614-8
; Sequence 8, Application US/09235614
; Patent No. 6183966
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: CLARK, CHRISTOPHER L.
; TITLE OF INVENTION: AN APPARATUS AND METHOD FOR SELECTIVELY RANKING
; TITLE OF INVENTION: SEQUENCES FOR ANTISENSE TARGETING
; FILE REFERENCE: 91556/66384
; CURRENT APPLICATION NUMBER: US/09/235,614
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/808,474
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 08/320,507
; PRIOR FILING DATE: 1994-10-07
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid mRNA
US-09-235-614-8

Query Match 100.0%; Score 20; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||
DB 1 agagagagagagagagagag 20

RESULT 10

TELEPHONE: (610) 454-3816
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "Oligonucleotide"
 US-08-860-038-19

Query Match 100.0%; Score 20; DB 4; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 20
 Db 26 AGAGAGAGAGAGAGAG 7

RESULT 12

US-09-580-923-19/c
 Sequence 19, Application US/09580923

Patent No. 6319672

GENERAL INFORMATION:

APPLICANT: Crouzet, Joel

APPLICANT: Scherman, Daniel

APPLICANT: Wils, Pierre

APPLICANT: Cameron, Beatrice

APPLICANT: Blanche, Francis

TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN

IMMOBILIZED OLIGONUCLEOTIDE

FILE REFERENCE: 03804.0138-01

CURRENT APPLICATION NUMBER: US/09/580,923

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 08/860,038

PRIOR FILING DATE: 1997-06-09

PRIOR APPLICATION NUMBER: PCT/FR95/01458

PRIOR FILING DATE: 1995-11-08

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 26

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: oligonucleotide

US-09-580-923-19

Query Match 100.0%; Score 20; DB 4; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 20
 Db 26 AGAGAGAGAGAGAGAG 7

RESULT 13

US-08-946-138-1

Sequence 1, Application US/08946138

Patent No. 6013445

GENERAL INFORMATION:

APPLICANT: Glenn Albrecht, Sydney Brenner, David H. Lloyd

TITLE OF INVENTION: Massively Parallel Signature Sequencing by

Ligation of Encoded Adaptors

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.

STREET: 3832 Bay Center Place
 CITY: Hayward
 STATE: California
 COUNTRY: USA
 ZIP: 94545
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Windows 3.1/DOS 5.0
 SOFTWARE: Microsoft Word for Windows, vers. 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/946,138
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/689,587
 FILING DATE: 12-AUG-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/659,453
 FILING DATE: 06-JUN-96
 ATTORNEY/AGENT INFORMATION:
 NAME: Stephen C. Macevitz
 REGISTRATION NUMBER: 30,285
 REFERENCE/DOCKET NUMBER: 808-1us
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 670-9365
 TELEFAX: (510) 670-9302
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-946-138-1

Query Match 100.0%; Score 20; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 20
 Db 9 AGAGAGAGAGAGAGAGAG 28

RESULT 14

US-09-225-652-1

Sequence 1, Application US/09225652

Patent No. 6175002

GENERAL INFORMATION:

APPLICANT: Robert B. DuBridge, Glen Albrecht, Sydney Brenner,

APPLICANT: Sergei M. Gryaznov, Sarah N. McCurdy

TITLE OF INVENTION: Adaptor-Based Sequence Analysis

Patent No. 6175002

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: Windows 3.1/DOS 5.0

SOFTWARE: Microsoft Word for Windows, vers. 2.0

CURRENT APPLICATION DATA:

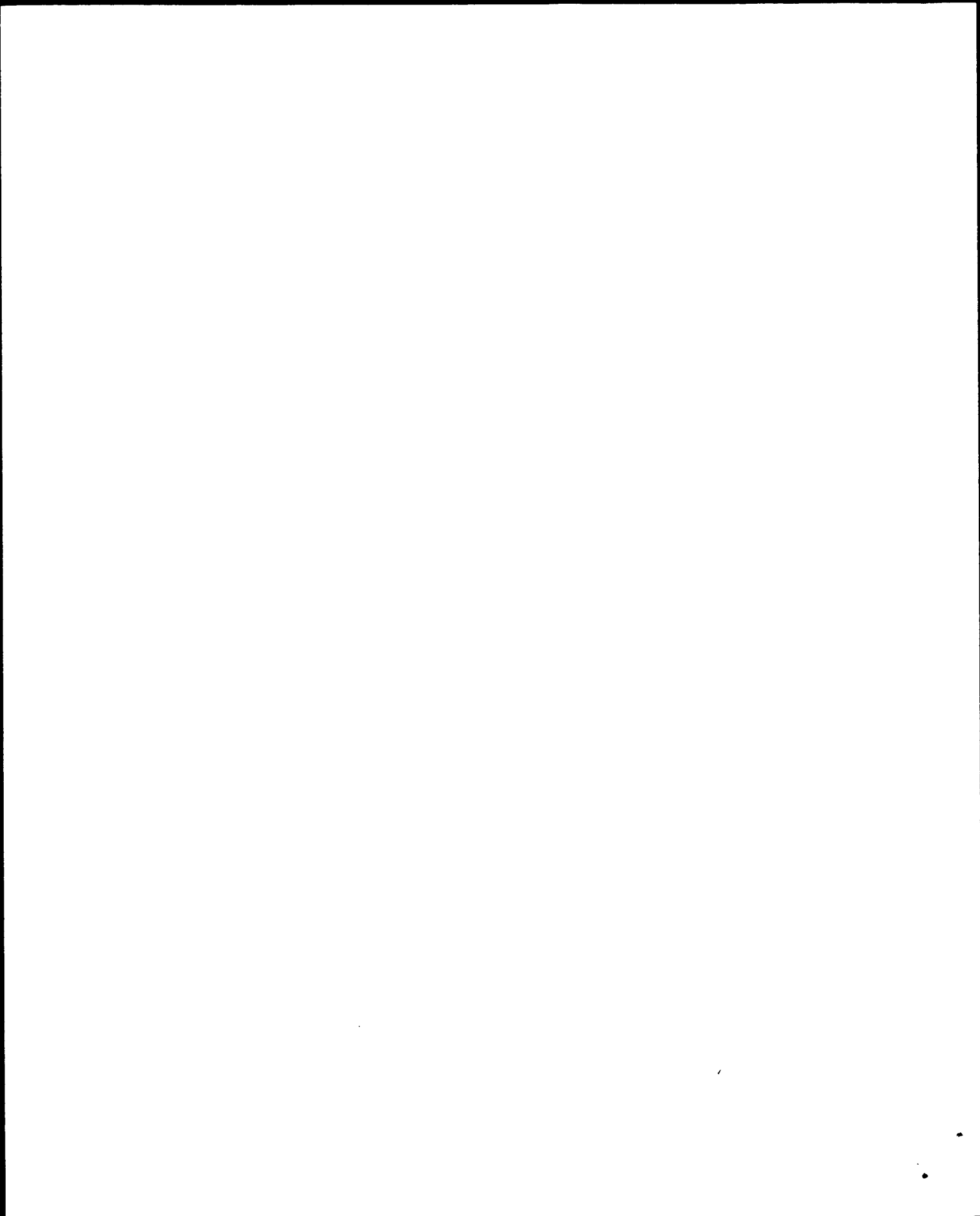
APPLICATION NUMBER: US/09/225,652

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/842,608



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 21:19:22 ; Search time 4810.92 Seconds
(without alignments)
56.110 Million cell updates/sec

Title: US-10-077-383-29

Perfect score: 20

Sequence: 1 agagagagagagagagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	20	12	AZ433566 1M0219C02
C 2	20	100.0	21	12	AZ394897 1M0158H11
C 3	20	100.0	21	12	AZ589098 1M0397B19
C 4	20	100.0	21	12	AZ627978 1M0476L04
C 5	20	100.0	22	12	AZ633751 1M0489J11
C 6	20	100.0	23	12	AZ822888 2M0096G06
C 7	20	100.0	25	12	AZ389918 1M015E05
C 8	20	100.0	25	12	AZ510124 1M0354K22
C 9	20	100.0	25	12	AZ659095 1M0536E18
C 10	20	100.0	25	12	AZ664804 1M0545H24
C 11	20	100.0	26	12	AZ342914 1M0076C22
C 12	20	100.0	26	12	AZ579594 1M0367O10
C 13	20	100.0	26	12	AZ641486 1M0504J06
C 14	20	100.0	26	12	AZ666145 1M0548C02
C 15	20	100.0	26	12	AZ771239 1M0573F15
C 16	20	100.0	26	12	AZ803946 2M0064P06
C 17	20	100.0	26	12	AZ813253 2M0080M20

c 18	20	100.0	26	12	AZ999813
c 19	20	100.0	27	12	AZ632991
c 20	20	100.0	27	12	AZ655531
c 21	20	100.0	27	12	AZ776487
c 22	20	100.0	27	12	AZ873739
c 23	20	100.0	28	12	AZ462549
c 24	20	100.0	28	12	AZ860136
c 25	20	100.0	28	12	AZ860136
c 26	20	100.0	29	12	AZ943199
c 27	20	100.0	29	12	AZ455946
c 28	20	100.0	30	12	AZ610578
c 29	20	100.0	31	12	AZ641732
c 30	20	100.0	31	12	AZ869598
c 31	20	100.0	32	12	AZ345558
c 32	20	100.0	32	12	AZ606035
c 33	20	100.0	32	12	AZ759124
c 34	20	100.0	33	12	AZ839021
c 35	20	100.0	33	12	AZ869302
c 36	20	100.0	33	12	AZ876021
c 37	20	100.0	33	12	AZ964180
c 38	20	100.0	34	10	AZ966687
c 39	20	100.0	35	10	BM047352
c 40	20	100.0	35	12	AZ956924
c 41	20	100.0	36	12	AZ387862
c 42	20	100.0	36	12	AZ664037
c 43	20	100.0	37	9	AV673465
c 44	20	100.0	37	12	AZ346663
c 45	20	100.0	37	12	AZ645311
					AZ803054

ALIGNMENTS

RESULT 1
AZ433566/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ433566
1M0219C02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0219C02 R, DNA sequence.
AZ433566
GSS
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0219 row: C column: 02
Seq primer: CACACAGGAAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0219C02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      0 a 10 c 0 g 10 t
ORIGIN

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Query Match      100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
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Db 20 AGAGAGAGAGAGAGAGAG 1

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```

RESULT 2
AZ394897/c
LOCUS      21 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION 1M0158H1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0158H1 R, DNA sequence.
ACCESSION  AZ394897
VERSION     AZ394897.1  GI:10509969
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
            and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0158 row: H column: 11
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES   source
            location/Qualifiers
            1..21
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0158H1"

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```

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      0 a 10 c 0 g 11 t
ORIGIN

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Query Match      100.0%; Score 20; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
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Db 21 AGAGAGAGAGAGAGAGAG 2

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RESULT 3
AZ589098
LOCUS      21 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION 1M0397B19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0397B19 R, DNA sequence.
ACCESSION  AZ589098
VERSION     AZ589098.1  GI:11711288
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
            and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0397 row: B column: 19
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES   source
            location/Qualifiers
            1..21
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"

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/clone="UUGCLM0397B19"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      11 a      0 c      10 g      0 t
ORIGIN

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Query Match      100.0%; Score 20; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagaagagagagagagag 20
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Db 1 AGAGAGAGAGAGAGAGAG 20

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RESULT 4
AZ627978/c
LOCUS      21 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION 1M0476104F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0476L04 F, DNA sequence.
ACCESSION  AZ627978
VERSION     AZ627978.1  GI:11750168
KEYWORDS   GSS
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: L column: 04
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES             source
    source
        1. 21
            /organism="Mus musculus"
            /strain="C57BL/6J"

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/db_xref="taxon:10090"
/clone="UUGCLM0476L04"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      10 c      0 g      11 t
ORIGIN

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```

Query Match      100.0%; Score 20; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagaagagagagagagag 20
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Db 21 AGAGAGAGAGAGAGAGAG 21

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```

RESULT 5
AZ633751/c
LOCUS      22 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION 1M0489111F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0489111 F, DNA sequence.
ACCESSION  AZ633751
VERSION     AZ633751.1  GI:11755941
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0489 row: I column: 11
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES             source
    source
        1. 22
            /organism="Mus musculus"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M048911"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1147321141gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      11 c      0 g      11 t
ORIGIN
Query Match      100.0%; Score 20; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
    |||||
Db 21 AGAGAGAGAGAGAGAGAG 2

RESULT 6
LOCUS   A2822888      23 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0096G06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0096G06 R, DNA sequence.
ACCESSION A2822888
VERSION   A2822888.1 GI:12992796
KEYWORDS GSS.
SOURCE    house mouse.
ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0096 row: G column: 06
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
            Location/Qualifiers
            source          1..23

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0096G06"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1147321141gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      11 a      0 c      12 g      0 t
ORIGIN
Query Match      100.0%; Score 20; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
    |||||
Db 2 AGAGAGAGAGAGAGAGAG 21

RESULT 7
LOCUS   A2389918      25 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION 1M0151E05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0151E05 F, DNA sequence.
ACCESSION A2389918
VERSION   A2389918.1 GI:10503626
KEYWORDS GSS.
SOURCE    house mouse.
ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 25)
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0151 row: E column: 05
            Seq primer: CGTGTAAACACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
            Location/Qualifiers
            FEATURES

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source
1. .25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0151E05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT      1 a 12 c 1 g 11 t
ORIGIN

Query Match      100.0%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 20
|||||
Db 25 AGAGAGAGAGAGAGAGAG 6

RESULT 8
AZ510124/c
LOCUS
DEFINITION      25 bp DNA linear GSS 05-OCT-2000
1M0354K22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0354K22 F, DNA sequence.
ACCESSION      AZ510124
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0354 row: K column: 23
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25

FEATURES
source
1. .25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0354K22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT      0 a 12 c 0 g 13 t
ORIGIN

Query Match      100.0%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 20
|||||
Db 25 AGAGAGAGAGAGAGAGAG 6

RESULT 9
AZ659095
LOCUS
DEFINITION      25 bp DNA linear GSS 14-DEC-2000
1M0536E18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0536E18 F, DNA sequence.
ACCESSION      AZ659095
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0536 row: E column: 18
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends

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Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
FEATURES
  source
    1. .25
      /organism="Mus musculus"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0545H24"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114[gbl]AFL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      12 a      0 c      13 g      0 t
ORIGIN
Query Match      100.0%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||
Db 3 AGAGAGAGAGAGAGAGAG 22

RESULT 10
AZ664804/c
LOCUS
DEFINITION
  1M0545H24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0545H24 F, DNA sequence.
ACCESSION
  AZ664804
VERSION
  AZ664804.1 GI:11801950
KEYWORDS
  GSS.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 25)
REFERENCE
  AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
    M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
    and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Robert B. Weiss
    University of Utah
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0545 row: H column: 24
    Seq primer: CGTTGTAACAGACGCCAGT

Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
FEATURES
  source
    1. .25
      /organism="Mus musculus"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0545H24"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114[gbl]AFL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      12 a      0 c      13 g      0 t
ORIGIN
Query Match      100.0%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
|||||
Db 3 AGAGAGAGAGAGAGAGAG 22

RESULT 11
AZ342914/c
LOCUS
DEFINITION
  1M0076C22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0076C22 F, DNA sequence.
ACCESSION
  AZ342914
VERSION
  AZ342914.1 GI:10420628
KEYWORDS
  GSS.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 26)
REFERENCE
  AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
    M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
    and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Robert B. Weiss
    University of Utah
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0076 row: C column: 22

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Seq primer: CGTTGTAACGAGCGGCAGT
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
 1. .26

FEATURES

source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0076C32"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 11 c 1 g 11 t
 ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
 |||||
 Db 26 AGAGAGAGAGAGAGAGAG 7

RESULT 12

AZ579594
 LOCUS 1M0367010F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0367010 F, DNA sequence.

ACCESSION AZ579594
 VERSION AZ579594.1 GI:11694023

KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0367 row: 0 column: 10
 Seq primer: CGTTGTAACGAGCGGCAGT
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
 1. .26

FEATURES

source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0367010"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 1 c 12 g 0 t
 ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagagag 20
 |||||
 Db 2 AGAGAGAGAGAGAGAGAG 21

RESULT 13

AZ641486
 LOCUS 1M0504J05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0504J06 F, DNA sequence.

ACCESSION AZ641486
 VERSION AZ641486.1 GI:11765514

KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0504 row: J column: 06
 Seq primer: CGTTGTAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers

FEATURES

source
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0504J06"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 0 a 13 c 0 g 13 t

Query Match 100.0%; Score 20; DB 12; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagagag 20
 |||||
 DB 25 AGAGAGAGAGAGAGAGAG 6

RESULT 14

AZ666145 26 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0548C02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION Clone UUGC1M0548C02 F, DNA sequence.
 ACCESSION AZ666145.1 GI:11803291
 VERSION GSS.
 KEYWORDS house mouse.
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

JOURNAL COMMENT

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0548 row: C column: 02
 Seq primer: CGTTGTAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers

FEATURES

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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 2 AGAGAGAGAGAGAGAGAG 21

RESULT 15

AZ771239 26 bp DNA linear GSS 16-FEB-2001
 LOCUS 1M0573F15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION Clone UUGC1M0573F15 F, DNA sequence.
 ACCESSION AZ771239.1 GI:12893285
 VERSION GSS.
 KEYWORDS house mouse.
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606

JOURNAL COMMENT

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 High quality sequence stop: 26.

FEATURES

Location/Qualifiers

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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
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 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 0 c 13 g 0 t
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 Best Local Similarity 100.0%; Pred. Nc. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: August 24, 2002, 21:19:25
 Job time: 20528 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 21:54:45 ; Search time 2108.3 Seconds
(without alignments)
198.516 Million cell updates/sec

Title: US-10-077-383-30

Perfect score: 20

Sequence: 1 nnnnnnnnnnnnnnnnnnnnn 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: gb_om.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ORGANISM	1	0	0.0	0.0	1	6	A95992	Sequence 25
REFERENCE	1	0	0.0	0.0	1	6	A95992	Sequence 25
AUTHORS	1	0	0.0	0.0	1	6	A95992	Sequence 25
TITLE	1	0	0.0	0.0	1	6	A95992	Sequence 25
JOURNAL	1	0	0.0	0.0	1	6	A95992	Sequence 25
FEATURES	1	0	0.0	0.0	1	6	A95992	Sequence 25
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SUMMARIES

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 n 1

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 ACCESSION A95992.1 GI:6779888
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 KEYWORDS
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 ORGANISM
 unclassified.
 unclassified.
 unclassified.
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 PIZZA, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
 TITLE
 JOURNAL
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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BASE COUNT 0 a 0 c 0 g 0 t 1 others
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QY 1 n 1
 Db 1 n 1

RESULT 3

A96002 A96002 1 bp DNA linear PAT 07-SEP-2000
 LOCUS Sequence 35 from Patent WO9924578.
 DEFINITION A96002
 ACCESSION A96002.1 GI:6779893
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified.
 unclassified.
 unclassified.
 1 (bases 1 to 1)
 PIZZA, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
 TITLE
 JOURNAL
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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BASE COUNT 0 a 0 c 0 g 0 t 1 others
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 Best Local Similarity 100.0%; Pred. No. 0;
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QY 1 n 1
 Db 1 n 1

Db 1 n 1

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 LOCUS Sequence 35 from Patent WO9924578.
 DEFINITION A96002
 ACCESSION A96002.1 GI:6779893
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified.
 unclassified.
 unclassified.
 1 (bases 1 to 1)
 PIZZA, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
 TITLE
 JOURNAL
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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 Best Local Similarity 100.0%; Pred. No. 0;
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 Db 1 n 1

RESULT 5

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 DEFINITION A96012
 ACCESSION A96012.1 GI:6779898
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified.
 unclassified.
 unclassified.
 1 (bases 1 to 1)
 PIZZA, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
 TITLE
 JOURNAL
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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BASE COUNT 0 a 0 c 0 g 0 t 1 others
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 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1
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RESULT 6

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 LOCUS Sequence 45 from Patent WO9924578.
 DEFINITION

ACCESSION A96012
 VERSION A96012.1 GI:6779898
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Pizza.M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 9924578-A 45 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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 Db 1 N 1
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 LOCUS A96022 1 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 55 from Patent WO9924578.
 ACCESSION A96022
 VERSION A96022.1 GI:6779903
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Pizza.M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 9924578-A 55 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 n 1
 Db 1 N 1
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 LOCUS A96022/c 1 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 55 from Patent WO9924578.
 ACCESSION A96022
 VERSION A96022.1 GI:6779903
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1)

AUTHORS Pizza.M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 9924578-A 55 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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 Db 1 N 1
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 LOCUS A96040 1 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 73 from Patent WO9924578.
 ACCESSION A96040
 VERSION A96040.1 GI:6779912
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Pizza.M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 9924578-A 73 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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 Db 1 N 1
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 DEFINITION Sequence 73 from Patent WO9924578.
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 VERSION A96040.1 GI:6779912
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Pizza.M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 9924578-A 73 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
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Db	1	N	1

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VERSION	A96058.1 GI:6779921
KEYWORDS	.
SOURCE	unidentified.
ORGANISM	unidentified. unclassified.
REFERENCE	1 (bases 1 to 1)
AUTHORS	Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE	Neserrial antigens
JOURNAL	Patent: WO 924578-A 91 20-MAY-1999;
	PIZZA MARIA GRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
	CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

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Best Local Similarity 100.0%; Pred. No. 0;
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Db	1	N	1

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VERSION	A96058.1 GI:6779921
KEYWORDS	.
SOURCE	unidentified.
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 1)
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TITLE	Nelisserial antigens
JOURNAL	Patent: WO 9924578-A 91 20-MAY-1999;
	PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
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VERSION	A96076.1 GI:6779930
KEYWORDS	.
SOURCE	unidentified.
ORGANISM	unidentified unclassified.
REFERENCE	1 (bases 1 to 1)
AUTHORS	Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE	Neisserial antigens
JOURNAL	Patent: WO 924578-A 109 20-MAY-1999; PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT); CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT) Location/Qualifiers
FEATURES	

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db 1 N 1

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ORGANISM	unidentified. unidentified unclassified.
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AUTHORS	Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE	Neisserial antigens
JOURNAL	Patent: WO 924578-A 109 20-MAY-1999; PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT); CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT) Location/Qualifiers
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DEFINITION  Sequence 119 from Patent WO9921578.
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KEYWORDS    .
SOURCE      unidentified.
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            unclassified.
            1 (bases 1 to 1)
REFERENCE   1  (bases 1 to 1)
AUTHORS     Piza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE       Neisserial antigens
JOURNAL     Patent: WO 9924578-A 119 20-MAY-1999;
            PIZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
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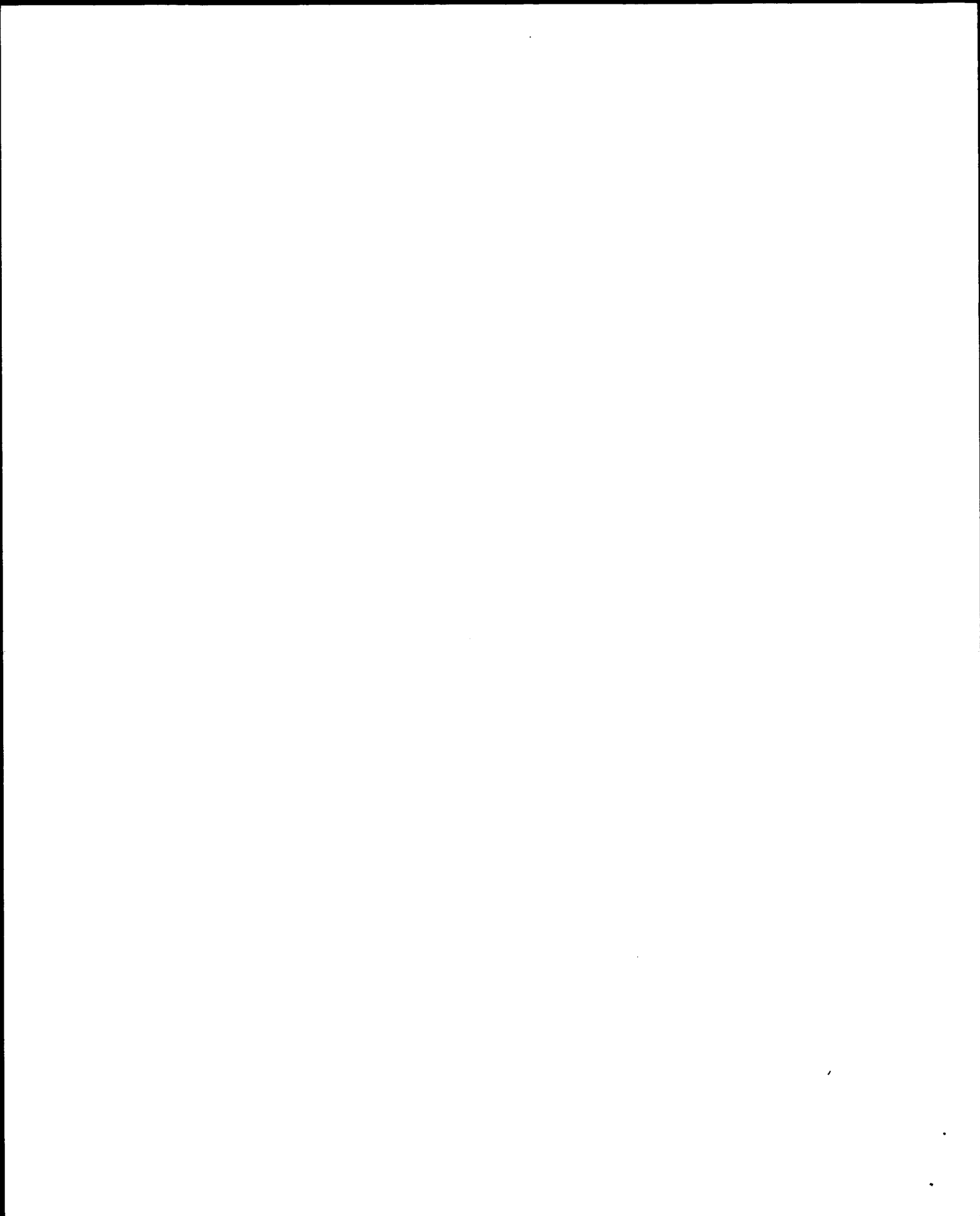
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Search completed: August 24, 2002, 21:54:45
 Job time: 22408 sec



PT Nucleic acid encoding potassium channels KCNQ2 and 3
 XX Claim 65; Page 151; 195pp; English.

CC This invention describes novel human and mouse potassium channel
 CC proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode
 CC KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for
 CC diagnosis and prognosis of benign familial neonatal epilepsy (BFNE),
 CC juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or
 CC transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the
 CC proteins themselves in cell-free form) are used to screen for agents that
 CC can be used to treat or prevent these forms of epilepsy. Fragments of the
 CC encoding nucleic acids are used as probes or primers, either for
 CC detecting mutations or for isolation of related sequences, while the
 CC complete sequences may be used in gene therapy to provide wild-type
 CC protein. Antibodies specific for mutant or wild-type proteins are used
 CC as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins
 CC are useful in rational design of drugs and therapeutically (in
 CC replacement therapies). The forms of epilepsy associated with mutations
 CC in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are
 CC manifest), and better treatment options will be available.
 CC AAX57074-X57139 are primers used in the method of the invention.
 XX Sequence 1 BP; 1 A; 0 C; 0 G; 0 U; 0 other;

Query Match 0.0%; Score 0; DB 20; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
 Db 1 a 1

RESULT 2
 AAX57131/C
 ID AAX57131 standard; DNA; 1 BP.

XX AAX57131;

XX 22-JUL-1999 (first entry)

XX Human mutant KCNQ3 primer 26.

XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
 KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
 KW detection; gene therapy; drug screening; primer; ss.

XX Synthetic.
 OS Homo sapiens.

XX WO9921875-A1.

XX 06-MAY-1999.

XX 23-OCT-1998; 98WO-US22375.

XX 24-OCT-1997; 97US-0063147.

XX (UTAH) UNIV UTAH RES FOUND.

XX Charlier C, Leppert MF, Singh NA;

XX WPI; 1999-312938/26.

PT Nucleic acid encoding potassium channels KCNQ2 and 3

XX Claim 65; Page 151; 195pp; English.

XX This invention describes novel human and mouse potassium channel
 CC proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode

CC KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for
 CC diagnosis and prognosis of benign familial neonatal epilepsy (BFNE),
 CC juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or
 CC transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the
 CC proteins themselves in cell-free form) are used to screen for agents that
 CC can be used to treat or prevent these forms of epilepsy. Fragments of the
 CC encoding nucleic acids are used as probes or primers, either for
 CC detecting mutations or for isolation of related sequences, while the
 CC complete sequences may be used in gene therapy to provide wild-type
 CC protein. Antibodies specific for mutant or wild-type proteins are used
 CC as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins
 CC are useful in rational design of drugs and therapeutically (in
 CC replacement therapies). The forms of epilepsy associated with mutations
 CC in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are
 CC manifest), and better treatment options will be available.
 CC AAX57074-X57139 are primers used in the method of the invention.

XX Sequence 1 BP; 1 A; 0 C; 0 G; 0 U; 0 other;

Query Match 0.0%; Score 0; DB 20; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1

Db 1 T 1

RESULT 3

AAN80743

ID AAN80743 standard; DNA; 3 BP.

XX AAN80743;

XX 10-SEP-1990 (first entry)

XX Sequence encoding complete mature and precursor forms of human tissue
 DE factor heavy chain proteins (hufh & pre-hufh, respectively).

XX Human tissue factor heavy chain (hufh); immunoassays;

KW precursor human tissue factor heavy chain (pre-hufh);

KW human tissue factor detection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 34..921

FT /*tag= a

FT /product=pre-hufh

FT 130..921

FT /*tag= b

FT /product=hufh

XX WO8807543-A.

XX 06-OCT-1988.

XX 29-MAR-1988; 88WO-US00998.

XX 25-JUN-1987; 87US-0067103.

XX (SCRI-) SCRIPPS CLINIC RES.

XX Eddington TS, Morrissey JH;

XX WPI; 1988-292837/41.

XX P-PSDB; AAP80713.

XX New DNA segment -

PT has gene encoding human tissue factor heavy chain protein and is

PT useful for inhibiting coagulation

XX

PS Disclosure; ; pp: English.

CC A DNA segment with a nucleotide sequence from about 130 to about 918 of the sequence given here is claimed. Also claimed are antibodies which immunoreact with hutfh and the claimed peptides (given in AAP80713). The antibodies may be used in immunoassays for detection of hutfh. The claimed peptides may be used to inhibit the binding of hutfh to coagulation factor VII/VIIa in vivo.

SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 n 1

RESULT 4
AAN80743/C

ID AAN80743 standard; DNA: 3 BP.

XX AAN80743;

XX 10-SEP-1990 (first entry)

DE Sequence encoding complete mature and precursor forms of human tissue factor heavy chain proteins (hutfh & pre-hutfh, respectively).

XX Human tissue factor heavy chain (hutfh); immunoassays;
KW precursor human tissue factor heavy chain (pre-hutfh);
KW human tissue factor detection.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 34..921
FT ' /*tag= a
FT /product=pre-hutfh
FT mat_peptide 130..921
FT /*tag= b
FT /product=hutfh

XX WO8807543-A.

XX 06-OCT-1988.

XX 29-MAR-1988; 88WO-0500998.

XX 25-JUN-1987; 87US-0067103.

XX (SCRIPT-) SCRIPPS CLINIC RES.

XX Eddington TS, Morrissey JH;
WPI: 1988-292837/41.
P-PSDB; AAP80713.

XX New DNA segment -
PT has gene encoding human tissue factor heavy chain protein and is
PT useful for inhibiting coagulation

XX Disclosure; ; pp: English.

CC A DNA segment with a nucleotide sequence from about 130 to about 918 of the sequence given here is claimed. Also claimed are antibodies which immunoreact with hutfh and the claimed peptides (given in AAP80713). The antibodies may be used in immunoassays for detection of hutfh. The claimed peptides may be used to inhibit the binding of hutfh to coagulation factor VII/VIIa in vivo.

XX SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
Db 3 N 3

RESULT 5
AAQ85491

ID AAQ85491 standard; cDNA: 3 BP.

XX AAQ85491;

XX 18-AUG-1995 (first entry)

DE Plasmid pEZ2318.thy2.

XX OMTKY3; turkey ovomucoid third domain peptide inhibitor;
KW furin inhibitor; protease inhibitor; pEZ2318.thy2; probe;
KW Escherichia coli; ss.
XX Synthetic.
XX WO9502055-A.
XX 19-JAN-1995.
XX 08-JUL-1994; 94WO-US07779.
XX 09-JUL-1993; 93US-0089248.
XX (ANDE/) ANDERSON S.
XX (LASK/) LASKOWSKI M.
XX Anderson S, Laskowski M;
XX WPI: 1995-066900/09.
XX Protein inhibitors of serine proteinase(s), e.g. furin, deriv.
PT from turkey ovomucoid third domain - used as laboratory reagents
PT to study the proteinase(s), or as chemotherapeutic agents to
PT treat diseases associated with them
XX Disclosure; Page 42-45; 66pp; English.

XX In synthetic analogs of turkey ovomucoid domain protein (6-56) (OMTKY3), given in AAR69818-24, the region immediately adjacent to the reactive site peptide bond is mutated to include the consensus sequence of furin or other serine protease. Polynucleotides encoding such analogs are incorporated into pEZ2318.thy2 and expressed in Escherichia coli RV308 (ATCC 31608).

XX SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 16; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 n 1

RESULT 6
AAQ85491/C

ID AAQ85491 standard; cDNA: 3 BP.

XX AAQ85491;
 AC
 XX 18-AUG-1995 (first entry)
 DT
 XX Plasmid PEZ2318.thy2.
 DE
 XX OMTK3; turkey ovomucoid third domain peptide inhibitor;
 KW furin inhibitor; protease inhibitor; PEZ2318.thy2; probe;
 KW Escherichia coli; ss.
 XX
 OS Synthetic.
 XX
 XX WO9502055-A.
 PN
 XX 19-JAN-1995.
 PD
 XX 08-JUL-1994; 94WO-US07779.
 PF
 XX 09-JUL-1993; 93US-0089248.
 PR
 XX (ANDE/) ANDERSON S.
 PA (LASK/) LASKOWSKI M.
 PI Anderson S, Laskowski M;
 XX
 PI WPI; 1995-066900/09.
 DR
 XX Protein inhibitors of serine proteinase(s), e.g. furin, deriv.
 PT from turkey ovomucoid third domain - used as laboratory reagents
 PT to study the proteinase(s), or as chemotherapeutic agents to
 PT treat diseases associated with them
 XX
 XX Disclosure; Page 42-45; 66pp; English.
 PS
 XX In synthetic analogs of turkey ovomucoid domain protein (6-56)
 CC (OMTK3), given in AAR69818-24, the region immediately adjacent to
 CC the reactive site peptide bond is mutated to include the consensus
 CC sequence of furin or other serine protease. Polynucleotides
 CC encoding such analogs are incorporated into PEZ2318.thy2 and
 CC expressed in Escherichia coli RV308 (ATCC 31608).
 XX
 XX Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;
 SQ

Query Match 0.0%; Score 0; DB 16; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
 Db 3 N 3

RESULT 7
 AAT33326
 ID AAT33326 standard; RNA; 3 BP.
 XX
 AC AAT33326;
 XX
 XX 12-NOV-1996 (first entry)
 DT
 XX CAPL trinucleotide.
 DE
 XX CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
 KW osteosarcoma; therapy; ss.
 XX
 OS Synthetic.
 XX
 XX WO9625499-A1.
 PN
 XX 22-AUG-1996.
 PD
 XX 16-FEB-1996; 96WO-US02108.
 PF
 XX 17-FEB-1995; 95US-0391375.
 PR
 XX (HYBR-) HYBRIDON INC.
 PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
 XX
 XX Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
 PI Von Hofe E;
 XX
 XX WPI; 1996-393400/39.
 DR
 XX Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
 PT useful to inhibit metastatic cancer, partic. osteosarcoma
 XX
 XX Claim 2; Page 56; 70pp; English.
 PS
 XX 22-AUG-1996.
 PD
 XX

PF 16-FEB-1996; 96WO-US02108.
 XX
 PR 17-FEB-1995; 95US-0391375.
 XX
 PA (HYBR-) HYBRIDON INC.
 XX
 XX (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
 PA
 XX Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
 PI Von Hofe E;
 XX
 XX WPI; 1996-393400/39.
 DR
 XX Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
 PT useful to inhibit metastatic cancer, partic. osteosarcoma
 XX
 XX Claim 2; Page 56; 70pp; English.
 PS
 XX Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5',
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.
 XX
 XX Sequence 3 BP; 0 A; 1 C; 1 G; 1 U; 0 other;
 SQ

Query Match 0.0%; Score 0; DB 17; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 c 1

RESULT 8
 AAT33326/C
 ID AAT33326 standard; RNA; 3 BP.
 XX
 AC AAT33326;
 XX
 XX 12-NOV-1996 (first entry)
 DT
 XX CAPL trinucleotide.
 DE
 XX CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
 KW osteosarcoma; therapy; ss.
 XX
 OS Synthetic.
 XX
 XX WO9625499-A1.
 PN
 XX 22-AUG-1996.
 PD
 XX 16-FEB-1996; 96WO-US02108.
 PF
 XX 17-FEB-1995; 95US-0391375.
 PR
 XX (HYBR-) HYBRIDON INC.
 PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
 XX
 XX Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
 PI Von Hofe E;
 XX
 XX WPI; 1996-393400/39.
 DR
 XX Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
 PT useful to inhibit metastatic cancer, partic. osteosarcoma
 XX
 XX Claim 2; Page 56; 70pp; English.
 PS
 XX

CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5'
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.
 XX Sequence 3 BP; 0 A; 1 C; 1 G; 1 U; 0 other;
 SQ

Query Match 0.0%; Score 0; DB 17; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 3 C 3

RESULT 9
 AAA94655
 ID AAA94655 standard; DNA; 3 BP.
 XX
 AC AAA94655;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Human TUB gene probe #2.
 XX
 KW Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;
 KW TUB; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6114502-A.
 XX
 PD 05-SEP-2000.
 XX
 PF 27-FEB-1998; 98US-0032365.
 XX
 PR 22-AUG-1996; 96US-0701380.
 PR 04-SEP-1996; 96US-0706292.
 PR 10-APR-1996; 96US-0630592.
 PR 17-SEP-1996; 96US-0714991.
 PR 30-APR-1997; 96US-0850218.
 PR 01-AUG-1997; 97US-0904699.
 PR 17-SEP-1997; 97US-0932306.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI North M, Nishina P, Noben-Trauth K, Naggert J;
 XX
 DR WPI; 2000-586483/55.
 XX
 PS Mammalian proteins expressed in retina and brain, useful for producing
 PT antibodies and for diagnosing neurosensory defects including cochlear
 PT degeneration, peripheral retinal degeneration and cone-rod retinal
 PT dystrophy -
 XX
 PS Disclosure; Columns 81-82; 61pp; Engl.sh.
 XX
 CC The present invention relates to human and murine cDNAs from a
 CC neurosensory defect associated gene family. The novel cDNAs are mouse
 CC tub form I (see AAA94629), mouse tub form II (see AAA94630), human TUB
 CC form 6 (see AAA94632), human TUB form 1 (see AAA94633), human TULP1 (see
 CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
 CC immunogens to raise antibodies that specifically identify TUB/TULP
 CC expressing cells and in drug screening assays directed at neurosensory
 CC defects. The novel proteins encoded by the present sequence can be used
 CC for the treatment of neurosensory degenerative conditions e.g. retinal
 CC dystrophies. The present sequence is a probe used to isolate the novel

CC genes of the present invention.
 XX
 SQ Sequence 3 BP; 0 A; 0 C; 3 G; 0 U; 0 other;
 Query Match 0.0%; Score 0; DB 21; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 g 1

RESULT 10
 AAA94655/c
 ID AAA94655 standard; DNA; 3 BP.
 XX
 AC AAA94655;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Human TUB gene probe #2.
 XX
 KW Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;
 KW TUB; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6114502-A.
 XX
 PD 05-SEP-2000.
 XX
 PF 27-FEB-1998; 98US-0032365.
 XX
 PR 22-AUG-1996; 96US-0701380.
 PR 04-SEP-1996; 96US-0706292.
 PR 10-APR-1996; 96US-0630592.
 PR 17-SEP-1996; 96US-0714991.
 PR 30-APR-1997; 97US-0850218.
 PR 01-AUG-1997; 97US-0904699.
 PR 17-SEP-1997; 97US-0932306.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI North M, Nishina P, Noben-Trauth K, Naggert J;
 XX
 DR WPI; 2000-586483/55.
 XX
 PS Mammalian proteins expressed in retina and brain, useful for producing
 PT antibodies and for diagnosing neurosensory defects including cochlear
 PT degeneration, peripheral retinal degeneration and cone-rod retinal
 PT dystrophy -
 XX
 PS Disclosure; Columns 81-82; 61pp; English.
 XX
 CC The present invention relates to human and murine cDNAs from a
 CC neurosensory defect associated gene family. The novel cDNAs are mouse
 CC tub form I (see AAA94629), mouse tub form II (see AAA94630), human TUB
 CC form 6 (see AAA94632), human TUB form 1 (see AAA94633), human TULP1 (see
 CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
 CC immunogens to raise antibodies that specifically identify TUB/TULP
 CC expressing cells and in drug screening assays directed at neurosensory
 CC defects. The novel proteins encoded by the present sequence can be used
 CC for the treatment of neurosensory degenerative conditions e.g. retinal
 CC dystrophies. The present sequence is a probe used to isolate the novel
 CC genes of the present invention.
 XX
 SQ Sequence 3 BP; 0 A; 0 C; 3 G; 0 U; 0 other;

Query Match 0.0%; Score 0; DB 21; Length 3;

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 3 C 3

RESULT 11
AAL20244
ID AAL20244 standard; cDNA; 3 BP.
XX
AC AAL20244;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 12701.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
XX
PR 14-MAR-2000; 2000US-0189167.
XX
PR 24-MAR-2000; 2000US-0192099.
XX
PR 29-MAR-2000; 2000US-0193480.
XX
PR 15-MAY-2000; 2000US-0205230.
XX
PR 09-JUN-2000; 2000US-0211315.
XX
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
PF WPI; 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS Claim 1; Page 2245; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

Query Match 0.0%; Score 0; DB 22; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 3 A 3

RESULT 13
AAL07544
ID AAL07544 standard; RNA; 4 BP.
XX
AC AAL07544;
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
XX metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO9500528-A.

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XX PD 05-JAN-1995.
XX XX
XX PF 17-JUN-1994; 94WO-US06884.
XX XX
XX PR 18-JUN-1993; 93US-0079677.
XX PR 07-JAN-1994; 94US-0179491.
XX XX
XX PA (PHAR-) PHARMAGENICS INC.
XX XX
XX PI Beutel BA, Joesten ME;
XX XX
XX DR WPI; 1995-051992/07.
XX XX
XX PT New oligo-nucleotide(s) that bind to basic fibroblast growth
XX PT factor - modulating, esp. inhibiting, its activity, useful in
XX PT treating cancer, preventing metastasis, and diagnosis.
XX PS Claim 3; Page 25; 44pp; English.
XX XX
XX CC The sequences given in AAQ81664-95 are oligonucleotides which modulate
XX CC the activity of basic fibroblast growth factor (bFGF) by binding
XX CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67
XX CC represent core sequences of which at least one is present in each of
XX CC the binding oligos. These oligonucleotides may form a single
XX CC strand, double strand, a stem-loop structure, a bubble structure, a
XX CC pseudoknot or a closed, circular structure. bFGF binds to high
XX CC affinity receptor and low affinity heparin-like molecules on the
XX CC cell surface. These oligonucleotides bind to bFGF in competition
XX CC with its receptor and heparin. These oligonucleotides may inhibit
XX CC or enhance the activity of bFGF. Particularly, they inhibit
XX CC neovascularisation so they can be used to suppress growth of solid
XX CC tumours and to reduce the risk of metastasis. They can be used as
XX CC diagnostic reagents to determine the presence of thrombin, or used in
XX CC gene therapy.
XX SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 16; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 g 1

RESULT 14
AAQ81664/c
ID AAQ81664 standard; RNA; 4 BP.
XX AC AAQ81664;
XX DT 29-SEP-1995 (first entry)
XX DE bFGF binding oligomer core sequence #1.
XX XX
XX KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
XX KW bubble structure; pseudoknot; receptor; heparin; competition;
XX KW inhibition; enhance; neovascularisation; solid tumour; cancer;
XX KW metastasis; diagnosis; gene therapy; ss.
XX OS Synthetic.
XX XX
XX PN WO9500528-A.
XX XX
XX PD 05-JAN-1995.
XX XX
XX PF 17-JUN-1994; 94WO-US06884.
XX XX
XX PR 18-JUN-1993; 93US-0079677.
XX PR 07-JAN-1994; 94US-0179491.
XX XX
XX PA (PHAR-) PHARMAGENICS INC.
XX XX
XX PI Beutel BA, Joesten ME;
XX XX
XX DR WPI; 1995-051992/07.
XX XX

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XX PA (PHAR-) PHARMAGENICS INC.
XX XX
XX PI Beutel BA, Joesten ME;
XX XX
XX DR WPI; 1995-051992/07.
XX XX
XX PT New oligo-nucleotide(s) that bind to basic fibroblast growth
XX PT factor - modulating, esp. inhibiting, its activity, useful in
XX PT treating cancer, preventing metastasis, and diagnosis.
XX PS Claim 3; Page 25; 44pp; English.
XX XX
XX CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
XX CC the activity of basic fibroblast growth factor (bFGF) by binding
XX CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67
XX CC represent core sequences of which at least one is present in each of
XX CC the binding oligos. These oligonucleotides may form a single
XX CC strand, double strand, a stem-loop structure, a bubble structure, a
XX CC pseudoknot or a closed, circular structure. bFGF binds to high
XX CC affinity receptor and low affinity heparin-like molecules on the
XX CC cell surface. These oligonucleotides bind to bFGF in competition
XX CC with its receptor and heparin. These oligonucleotides may inhibit
XX CC or enhance the activity of bFGF. Particularly, they inhibit
XX CC neovascularisation so they can be used to suppress growth of solid
XX CC tumours and to reduce the risk of metastasis. They can be used as
XX CC diagnostic reagents to determine the presence of thrombin, or used in
XX CC gene therapy.
XX SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 16; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 4 G 4

RESULT 15
AAQ81665
ID AAQ81665 standard; RNA; 4 BP.
XX AC AAQ81665;
XX DT 29-SEP-1995 (first entry)
XX DE bFGF binding oligomer core sequence #2.
XX XX
XX KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
XX KW bubble structure; pseudoknot; receptor; heparin; competition;
XX KW inhibition; enhance; neovascularisation; solid tumour; cancer;
XX KW metastasis; diagnosis; gene therapy; ss.
XX OS Synthetic.
XX XX
XX PN WO9500528-A.
XX XX
XX PD 05-JAN-1995.
XX XX
XX PF 17-JUN-1994; 94WO-US06884.
XX XX
XX PR 18-JUN-1993; 93US-0079677.
XX PR 07-JAN-1994; 94US-0179491.
XX XX
XX PA (PHAR-) PHARMAGENICS INC.
XX XX
XX PI Beutel BA, Joesten ME;
XX XX
XX DR WPI; 1995-051992/07.
XX XX

```

PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 PT factor - modulating, esp. inhibiting, its activity, useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp; English.
 XX
 CC The sequences given in AA081642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AA081664-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC with its receptor and heparin. These oligonucleotides may inhibit
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 16; Length 4;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
 Db 1 c 1

Search completed: August 24, 2002, 22:08:16
 Job time: 8849 sec

RESULT 2

PCT-US93-00977-702/c
 ; Sequence 702, Application PC/TUS9300977
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
 ; NUMBER OF SEQUENCES: 711
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson, and Bear
 ; STREET: 620 Newport Center Dr. Sixteenth Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/00977
 ; FILING DATE: 19930129
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Altman, Daniel E.
 ; REGISTRATION NUMBER: 34,115
 ; REFERENCE/DOCKET NUMBER: HITACHI.006H
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 714-760-0404
 ; TELEFAX: 714-760-9502
 ; INFORMATION FOR SEQ ID NO: 702:
 ; LENGTH: 1
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: gDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; PCT-US93-00977-702

Query Match 0.0%; Score 0; DB 5; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 t 1

RESULT 3

US-08-268-679B-8
 ; Sequence 8, Application US/08268679B
 ; Patent No. 5674729
 ; GENERAL INFORMATION:
 ; APPLICANT: WIMMER, ECKARD; MOLLA,
 ; APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.
 ; TITLE OF INVENTION: DE NOVO CELL-FREE
 ; TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 ; STREET: 345 PARK AVE.
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORD PERFECT # 5.1
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/268,679B
 ; FILING DATE: 30-JUN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07\846,914
 ; FILING DATE: 06-MAR-1992
 ; CLASSIFICATION: 435
 ; APPLICATION NUMBER: 07\719,761
 ; FILING DATE: 24-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MARIA C.H. LIN
 ; REGISTRATION NUMBER: 29,323
 ; REFERENCE/DOCKET NUMBER: 0887-4095 US2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4800
 ; TELEFAX: (212) 751-6849
 ; TELEX: 421792
 ; INFORMATION FOR SEQ ID NO: 8:
 ; LENGTH: 2
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: SINGLE
 ; TOPOLOGY: UNKNOWN
 ; MOLECULE TYPE:
 ; DESCRIPTION: OLIGONUCLEOTIDE
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: YES
 ; ORIGINAL SOURCE: N.A.
 ; POSITION IN GENOME: N.A.
 ; US-08-268-679B-8

Query Match 0.0%; Score 0; DB 1; Length 2;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 g 1

RESULT 4

US-08-268-679B-8/c
 ; Sequence 8, Application US/08268679B
 ; Patent No. 5674729
 ; GENERAL INFORMATION:
 ; APPLICANT: WIMMER, ECKARD; MOLLA,
 ; APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.
 ; TITLE OF INVENTION: DE NOVO CELL-FREE
 ; TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 ; STREET: 345 PARK AVE.
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORD PERFECT # 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/268,679B
 ; FILING DATE: 30-JUN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07\846,914
 ; FILING DATE: 06-MAR-1992
 ; CLASSIFICATION: 435
 ; APPLICATION NUMBER: 07\719,761
 ; FILING DATE: 24-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MARIA C.H. LIN

; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 0887-4095 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: OLIGONUCLEOTIDE
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE: N.A.
; POSITION IN GENOME: N.A.
US-08-268-679B-8

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 2 C 2

RESULT 5
US-08-457-274A-16
; Sequence 16, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; APPLICANT: Tomita, Takashi
; TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Musca domestica
; STRAIN: Learn-Pyr
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
US-08-457-274A-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 2 T 2

; STRAIN: Learn-Pyr
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
US-08-457-274A-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 A 1

RESULT 6
US-08-457-274A-16/c
; Sequence 16, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; APPLICANT: Tomita, Takashi
; TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Musca domestica
; STRAIN: Learn-Pyr
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
US-08-457-274A-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 2 T 2

```

RESULT 7
US-08-484-192-16
; Sequence 16, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1,**)
; OTHER INFORMATION: /note="This is a biotin-17
; OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-484-192-16

```

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Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 n 1
Db 1 n 1

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RESULT 8
US-08-484-192-16/c
; Sequence 16, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN

```

```

; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1,**)
; OTHER INFORMATION: /note="This is a biotin-17
; OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-484-192-16

```

```

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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Qy 1 n 1
Db 2 C 2

```

```

RESULT 9
US-08-726-464B-28
; Sequence 28, Application US/08726464B
; Patent No. 5932346
; GENERAL INFORMATION:

```

```

; APPLICANT: BARRETT, Ronald W.
; APPLICANT: DOWER, William J.
; APPLICANT: CWIRLA, Steven A.
; APPLICANT: JOHNSON, Sherril S.
; APPLICANT: WRIGHTON, Nicholas C.
; APPLICANT: DUFFIN, David J.
; APPLICANT: WAGSTROM, Christopher R.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO THE
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSER: TOWNSEND AND TOWNSEND AND CREW
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,464B
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-024100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/576-0200
; TELEFAX: 415/576-0300
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; US-08-726-464B-28

Query Match 0.0%; Score 0; DB 2; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 n 1
Db 1 v 1

RESULT 10
US-08-726-464B-28/c
; Sequence 28, Application US/08726464B
; Patent No. 5932546
; GENERAL INFORMATION:
; APPLICANT: BARRETT, Ronald W.
; APPLICANT: DOWER, William J.
; APPLICANT: CWIRLA, Steven A.
; APPLICANT: JOHNSON, Sherrill S.
; APPLICANT: WRIGHTON, Nicholas C.
; APPLICANT: DUFFIN, David J.
; APPLICANT: WAGSTROM, Christopher R.
; TITLE OF INVENTION: PETIDES AND COMPOUNDS THAT BIND TO THE
; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,464B
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-024100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/576-0200
; TELEFAX: 415/576-0300
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; US-08-726-464B-28

```

```

Query Match 0.0%; Score 0; DB 2; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

```

```

Qy 1 n 1
Db 2 y 2

```

```

RESULT 11
US-09-016-520-35
; Sequence 35, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; EARLIER FILING DATE: 1998-01-30
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
; US-09-016-520-35

```

```

Query Match 0.0%; Score 0; DB 3; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

```

```

Qy 1 n 1
Db 1 t 1

```

```

RESULT 12
US-09-016-520-35/c
; Sequence 35, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides

```

; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-35

Query Match 0.0%; Score 0; DB 3; Length 2;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 2 A 2

RESULT 13

US-09-130-973-35
; Sequence 35, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-35

Query Match 0.0%; Score 0; DB 4; Length 2;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 t 1

RESULT 14

US-09-130-973-35/c
; Sequence 35, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:

; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-35

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Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2 A 2

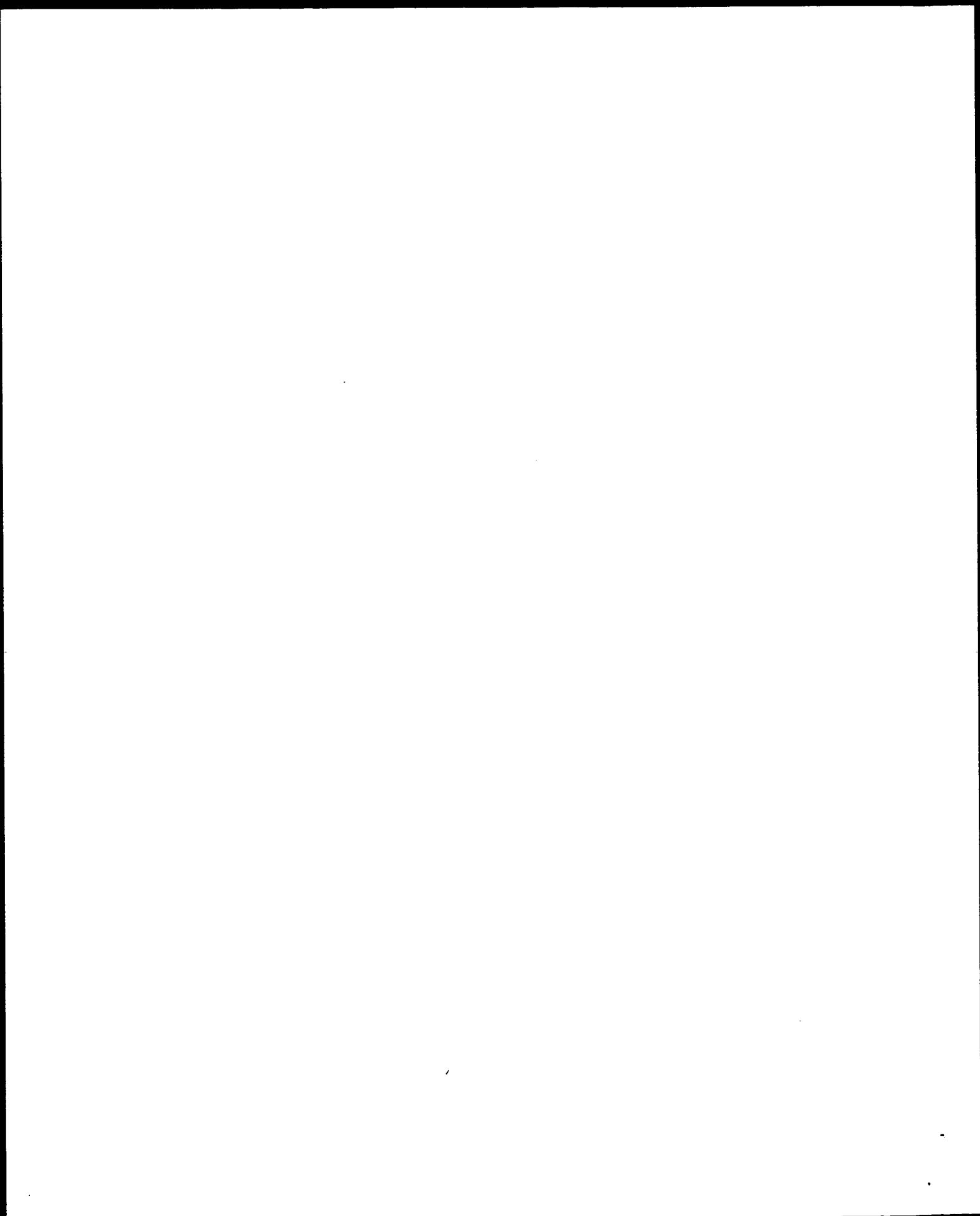
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US-09-477-902-35
; Sequence 35, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-477-902-35

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Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 t 1

Search completed: August 24, 2002, 21:57:39
Job time: 21597 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 21:19:25 ; Search time 4810.92 seconds
(without alignments)
56.110 Million cell updates/sec

Title: US-10-077-383-30

Perfect score: 20

Sequence: 1 nnnnnnnnnnnnnnnnnnnnn 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pin:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	0	0.0	1	2	HSW001740	AL037411 Homo sapi
3	0	0.0	1	2	HSW003869	AL039393 Homo sapi
4	0	0.0	1	2	HSW003869	AL039393 Homo sapi
5	0	0.0	1	2	HSW005008	AL040532 Homo sapi
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8	0	0.0	1	2	HSW011115	AL046265 Homo sapi
9	0	0.0	1	2	HSW011270	AL046420 Homo sapi
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c	22	0	0.0	1	10	BE402351
c	23	0	0.0	1	10	BE402374
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ALIGNMENTS

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AC AL037411;

SV AL037411.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp564L2071_s1 (from clone DKFZp564L2071)

DE EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RP 1-1

RA Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the ENBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitze 18a D-8152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by GBF within the cDNA

CC sequencing consortium of the German Genome Project

CC No r1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

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FT /clone_lib="564 (synonym: hibr2). Vector pAMP1; host

FT Xl-2blue; sites NotI + SalI"
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 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
 Db 1 C 1

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 ID HSM001740 standard; RNA; EST; 1 BP.

XX AC AL037411;
 XX SV AL037411.1
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 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA; EST DKFZp564L2071_s1 (from clone DKFZp564L2071)
 DE EST; expressed sequence tag.
 KW Homo sapiens (human)
 XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX [1]
 RN 1-1
 RA Bloeker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
 RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIFS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX Clone from S. Wiemann, sequenced by GBF within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No r1 sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

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Oy 1 n 1
 Db 1 G 1

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 XX AC AL039393;
 XX SV AL039393.1
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA; EST DKFZp434J0410_s1 (from clone DKFZp434J0410)
 DE EST; expressed sequence tag.
 KW Homo sapiens (human)
 XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX [1]
 RN 1-1
 RA Dueterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
 RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIFS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
 CC sequencing consortium of the German Genome Project
 CC r1 sequence also available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

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 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
 Db 1 A 1

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 XX SV AL039393.1
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 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA; EST DKFZp434J0410_s1 (from clone DKFZp434J0410)
 DE EST; expressed sequence tag.
 KW Homo sapiens (human)
 XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

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XX [1]
RN I-1
RA Duusterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC RI sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
DB 1 T 1

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AC AL040532;
XX
SV AL040532.1
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DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
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XX
KW EST; expressed sequence tag.
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OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
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XX
RN [1]
RP 1-1
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No SI sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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DB 1 T 1

RESULT 5
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XX
SV AL040532.1
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DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
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KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
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RP 1-1
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RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
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CC sequencing consortium of the German Genome Project
CC No SI sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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FH Key Location/Qualifiers

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QY 1 n 1
DB 1 C 1

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XX
SV AL040532.1
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DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
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KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-1
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No SI sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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Db      1 G 1

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DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
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KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-1
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 G 1

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SV AL046420.1
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DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
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XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-1
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
XX

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CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

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Qy 1 n 1
 Db 1 C 1

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 SV AL046420.1
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 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
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 DE EST: expressed sequence tag.
 KW
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 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX
 XX [1]

RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX
 XX Clone from S. Wiemann, sequenced by BMFZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No si sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

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Qy 1 n 1
 Db 1 G 1

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 ID HSW011922 standard; RNA; EST; 1 BP.

XX AC AL047072;
 XX SV AL047072.1

XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX

DE Homo sapiens mRNA; EST DKFZp586P0817_r1 (from clone DKFZp586P0817)
 DE EST: expressed sequence tag.
 KW
 KW Homo sapiens (human)
 OS
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX
 XX [1]
 RN
 RN 1-1
 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX
 XX Clone from S. Wiemann, sequenced by BMFZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No si sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX
 FH Key Location/Qualifiers
 FT source 1. .1
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp586P0817"
 FT /clone_lib="586 (synonym: htel). Vector pSport1; host
 FT DH10B; sites Noti + Sali/Wlul"
 FT /dev_stage="adult"
 FT /tissue_type="uterus"

XX Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 C 1

RESULT 12

HSW011922/c
 ID HSW011922 standard; RNA; EST; 1 BP.

XX AC AL047072;
 XX SV AL047072.1

DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 DE Homo sapiens mRNA; EST DKFZp586p0817_r1 (from clone DKFZp586p0817)
 XX EST; expressed sequence tag.
 KW
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX
 RN [1]
 RP 1-1
 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No sl sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX
 FH Key Location/Qualifiers
 FH source 1.1
 FT /db_xref="taxon:9606"
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 FT /clone_lib="586 (synonym: hutel). Vector pSport1; host
 FT DH10B; sites NotI + SalI/WluI"
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 FT /tissue_type="uterus"
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Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 G 1

RESULT 13
 BI416880 1 bp mRNA linear EST 15-AUG-2001
 LOCUS hasp002xj20f Heterobasidion annosum - Scots pine infection stage
 DEFINITION subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
 annosum cDNA clone hasp002xj20f, mRNA sequence.
 ACCESSION BI416880
 VERSION BI416880.1 GI:15187903
 KEYWORDS EST.
 SOURCE Pinus sylvestris/Heterobasidion annosum.
 ORGANISM Pinus sylvestris/Heterobasidion annosum.
 Eukaryota; mixed EST libraries.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
 TITLE Expressed sequence tags of randomly selected cDNA clones from the
 interaction of the root rot fungus (Heterobasidion annosum) with
 seedling roots of Scots pine (Pinus sylvestris)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Fred O. Asiegbu
 Dept. of Forest Mycology & Pathology
 Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,
 Sweden
 Tel: +46 18 67 15 98
 Fax: +46 18 30 92 45
 Email: Fred.Asiegbu@mykopat.slu.se
 Seq primer: T7 primer.
 Location/Qualifiers
 1.1
 /organism="Pinus sylvestris/Heterobasidion annosum"
 /db_xref="taxon:169015"
 /clone="hasp002xj20f"
 /clone_lib="Heterobasidion annosum - Scots pine infection
 stage subtraction cDNA library (hasp)"
 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
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 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (PP5)."
 BASE COUNT 0 a 0 c 0 g 0 t 1 others
 ORIGIN

Seq primer: T7 primer.
 Location/Qualifiers
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 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
 hybridization cDNA library was constructed from scots
 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (PP5)."
 BASE COUNT 0 a 0 c 0 g 0 t 1 others
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 N 1

RESULT 14
 BI416880/c 1 bp mRNA linear EST 15-AUG-2001
 LOCUS hasp002xj20f Heterobasidion annosum - Scots pine infection stage
 DEFINITION subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
 annosum cDNA clone hasp002xj20f, mRNA sequence.
 ACCESSION BI416880
 VERSION BI416880.1 GI:15187903
 KEYWORDS EST.
 SOURCE Pinus sylvestris/Heterobasidion annosum.
 ORGANISM Pinus sylvestris/Heterobasidion annosum.
 Eukaryota; mixed EST libraries.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
 TITLE Expressed sequence tags of randomly selected cDNA clones from the
 interaction of the root rot fungus (Heterobasidion annosum) with
 seedling roots of Scots pine (Pinus sylvestris)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Fred O. Asiegbu
 Dept. of Forest Mycology & Pathology
 Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,
 Sweden
 Tel: +46 18 67 15 98
 Fax: +46 18 30 92 45
 Email: Fred.Asiegbu@mykopat.slu.se
 Seq primer: T7 primer.
 Location/Qualifiers
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 /organism="Pinus sylvestris/Heterobasidion annosum"
 /db_xref="taxon:169015"
 /clone="hasp002xj20f"
 /clone_lib="Heterobasidion annosum - Scots pine infection
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 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
 hybridization cDNA library was constructed from scots
 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (PP5)."
 BASE COUNT 0 a 0 c 0 g 0 t 1 others
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Query Match 0.0%; Score 0; DB 10; Length 1;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 n 1
|
Db 1 n 1

RESULT 15

BI817896

LOCUS

DEFINITION

G3-023 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar

to Putative heterochromatin-like protein 1, mRNA sequence.

ACCESSION

BI817896

VERSION

BI817896.1

KEYWORDS

EST

SOURCE

axolotl.

ORGANISM

Ambystoma mexicanum

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;

Ambystoma.

REFERENCE

1 (bases 1 to 1)

AUTHORS

Voss,S.R., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,

Gardiner,D.M. and Parichy,D.M.

TITLE

Expressed sequence tags from an axolotl limb regeneration library

JOURNAL

Unpublished (2001)

COMMENT

Contact: Voss SR

Department of Biology

Colorado State University

Fort Collins, CO 80523, USA

Tel: 970 491 4869

Fax: 970 491 0849

Email: srvoss@amar.colostate.edu

Single pass sequence from 5' end. Low quality sequence was trimmed

from the ends (PHRED error rate = 5%). Trace file available:

srvoss@amar.colostate.edu.

Location/Qualifiers

1..1

source

/organism="Ambystoma mexicanum"

/db_xref="taxon:8296"

/clone_lib="Axolotl Lambda Zap Library"

/tissue_type="Regenerating forelimb"

/dev_stage="Medium-bud blastema"

BASE COUNT

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ORIGIN

Query Match

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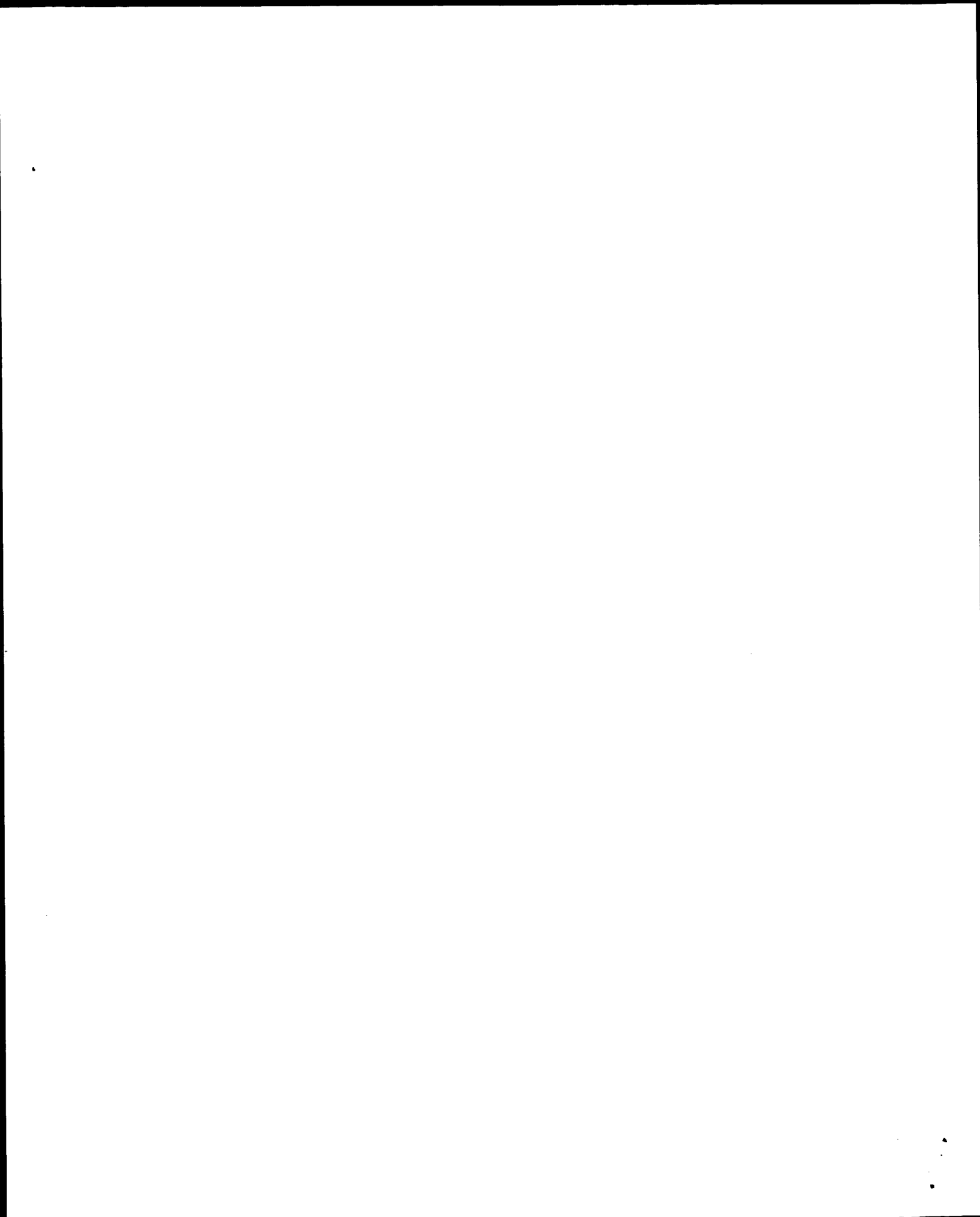
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Oy 1 n 1

Db 1 c 1

Search completed: August 24, 2002, 21:19:25

Job time: 20528 sec



Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 18 AGAGAGAGAGAGAGAG 1

RESULT 2
 AR069073/c
 LOCUS AR069073 20 bp DNA PAT 29-SEP-1999
 DEFINITION Sequence 23 from patent US 5854410.
 ACCESSION AR069073
 VERSION AR069073.1 GI:6001280
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Arnold, L.J. Jr., Reynolds, M.A., Schwartz, D.A. and Daily, W.J.
 TITLE Oligonucleoside cleavage compounds and therapies
 JOURNAL Patent: US 5854410-A 23 29-DEC-1998;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"

BASE COUNT 1 a 9 c 1 g 9 t
 ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
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 Db 19 AGAGAGAGAGAGAGAG 2

RESULT 3
 AR084583
 LOCUS AR084583 20 bp DNA PAT 01-SEP-2000
 DEFINITION Sequence 72 from patent US 5981185.
 ACCESSION AR084583
 VERSION AR084583.1 GI:10011354
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
 TITLE Oligonucleotide repeat arrays
 JOURNAL Patent: US 5981185-A 72 09-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"

BASE COUNT 10 a 0 c 10 g 0 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
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QY 1 agagagagagagagagag 18
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 Db 1 AGAGAGAGAGAGAGAG 18

RESULT 4
 AR084604/c
 LOCUS AR084604 20 bp DNA PAT 01-SEP-2000
 DEFINITION Sequence 93 from patent US 5981185.
 ACCESSION AR084604
 VERSION AR084604.1 GI:10011375

KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
 TITLE Oligonucleotide repeat arrays
 JOURNAL Patent: US 5981185-A 93 09-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..20
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BASE COUNT 0 a 10 c 0 g 10 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
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QY 1 agagagagagagagagag 18
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 Db 20 AGAGAGAGAGAGAGAG 3

RESULT 5
 IL16926/c
 LOCUS IL16926 20 bp DNA PAT 03-APR-1996
 DEFINITION Sequence 1 from patent US 5482836.
 ACCESSION IL16926
 VERSION IL16926.1 GI:1251834
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Cantor, C.R., Ito, T. and Smith, C.L.
 TITLE DNA purification by triplex-affinity capture and affinity capture electrophoresis
 JOURNAL Patent: US 5482836-A 1 09-JAN-1996;
 FEATURES Location/Qualifiers
 source 1..20
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BASE COUNT 0 a 10 c 0 g 10 t
 ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
 |||||
 Db 19 AGAGAGAGAGAGAGAG 2

RESULT 6
 A64735/c
 LOCUS A64735 21 bp DNA PAT 29-MAR-1999
 DEFINITION Sequence 1 from Patent WO9729116.
 ACCESSION A64735
 VERSION A64735.1 GI:4530771
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Reese, C.B. and Rao, M.V.
 TITLE SULPHUR CONTAINING DINUCLEOTIDE PHOSPHORAMIDITES
 JOURNAL Patent: WO 9729116-A 1 14-AUG-1997;
 FEATURES Location/Qualifiers
 source 1..21
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BASE COUNT 0 a 10 c 0 g 11 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagag 18
|||||
Db 21 AGAGAGAGAGAGAG 4

RESULT 7

A64736/c A64736 21 bp DNA linear PAT 29-MAR-1999
LOCUS
DEFINITION Sequence 2 from Patent WO9729116.
ACCESSION A64736
VERSION A64736.1 GI:4530772

KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Reese,C.B. and Rao,M.V.

TITLE SULPHUR CONTAINING DINUCLEOTIDE PHOSPHORAMIDITES
JOURNAL Patent: WO 9729116-A 2 14-AUG-1997;

CRUACHEM LTD (GB)
FEATURES Location/Qualifiers

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/db_xref="taxon:32644"
BASE COUNT 1 a 10 c 0 g 10 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagag 18
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Db 20 AGAGAGAGAGAGAG 3

RESULT 8

A64738/c A64738 21 bp DNA linear PAT 16-OCT-1999
LOCUS
DEFINITION Sequence 4 from Patent WO9729116.
ACCESSION A64738
VERSION A64738.1 GI:4530774

KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Reese,C.B. and Rao,M.V.

TITLE SULPHUR CONTAINING DINUCLEOTIDE PHOSPHORAMIDITES
JOURNAL Patent: WO 9729116-A 4 14-AUG-1997;

CRUACHEM LTD (GB)
FEATURES Location/Qualifiers

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagag 18
|||||
Db 21 AGAGAGAGAGAGAG 4

RESULT 9

A64739/c A64739 21 bp DNA linear PAT 16-OCT-1999
LOCUS
DEFINITION Sequence 5 from Patent WO9729116.
ACCESSION A64739
VERSION A64739.1 GI:4530775

KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Reese,C.B. and Rao,M.V.

TITLE SULPHUR CONTAINING DINUCLEOTIDE PHOSPHORAMIDITES
JOURNAL Patent: WO 9729116-A 5 14-AUG-1997;

CRUACHEM LTD (GB)
FEATURES Location/Qualifiers

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/db_xref="taxon:32644"
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modified_base 6

modified_base 8

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modified_base 12

modified_base 14

modified_base 16

modified_base 18

modified_base 20

BASE COUNT 1 a 10 c 0 g 10 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db      20 AGAGAGAGAGAGAGAG 3

RESULT 10
AX083691/c
LOCUS   AX083691
DEFINITION Sequence 5 from Patent WO0110468.
ACCESSION AX083691
VERSION  AX083691.1 GI:13185419
KEYWORDS
SOURCE  synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 21)
AUTHORS  Papisov,M.I.
TITLE    Drug-carrier complexes and methods of use thereof
JOURNAL  Patent: WO 0110468-A 5 15-FEB-2001;
        THE GENERAL HOSPITAL CORPORATION (US)
FEATURES
source  1..21
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        /db_xref="taxon:32630"
        /note="Synthetic Oligonucleotide"
BASE COUNT 0 a 9 c 0 g 12 t
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
    |||||||
Db 21 AGAGAGAGAGAGAGAG 4

RESULT 11
AX083696/c
LOCUS   AX083696
DEFINITION Sequence 10 from Patent WO0110468.
ACCESSION AX083696
VERSION  AX083696.1 GI:13185424
KEYWORDS
SOURCE  synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 21)
AUTHORS  Papisov,M.I.
TITLE    Drug-carrier complexes and methods of use thereof
JOURNAL  Patent: WO 0110468-A 10 15-FEB-2001;
        THE GENERAL HOSPITAL CORPORATION (US)
FEATURES
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        /note="Synthetic Oligonucleotide"
BASE COUNT 0 a 9 c 0 g 12 t
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
    |||||||
Db 21 AGAGAGAGAGAGAGAG 4

RESULT 12
AX083692
LOCUS   AX083692
DEFINITION Sequence 6 from Patent WO0110468.
ACCESSION AX083692
VERSION  AX083692.1 GI:13185420
KEYWORDS
SOURCE  synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS  Papisov,M.I.
TITLE    Drug-carrier complexes and methods of use thereof
JOURNAL  Patent: WO 0110468-A 6 15-FEB-2001;
        THE GENERAL HOSPITAL CORPORATION (US)
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BASE COUNT 13 a 0 c 9 g 0 t
ORIGIN

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
    |||||||
Db 1 AGAGAGAGAGAGAGAG 18

RESULT 13
AX104716/c
LOCUS   AX104716
DEFINITION Sequence 908 from Patent WO0122972.
ACCESSION AX104716
VERSION  AX104716.1 GI:13920913
KEYWORDS
SOURCE  synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS  Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE    Immunostimulatory nucleic acids
JOURNAL  Patent: WO 0122972-A 908 05-APR-2001;
        UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
        GmbH (DE)
FEATURES
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        /db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 AGAGAGAGAGAGAGAG 5

RESULT 14
AR026545
LOCUS   AR026545
DEFINITION Sequence 8 from patent US 5856103.
ACCESSION AR026545
VERSION  AR026545.1 GI:5937385
KEYWORDS
SOURCE  Unknown.
ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 24)
 AUTHORS Gray,D.M. and Clark,C.L.
 TITLE Method for selectively ranking sequences for antisense targeting
 JOURNAL Patent: US 5856103-A 8 05-JAN-1999;
 FEATURES Location/Qualifiers
 source 1..24
 /organism="unknown"

BASE COUNT 12 a 0 c 12 g 0 t
 ORIGIN

Query Match 100.0%; Score 13; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
 |||||
 Db 1 AGAGAGAGAGAGAGAG 18

RESULT 15
 AR026546/c
 LOCUS AR026546 24 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 9 from patent US 5856103.
 ACCESSION AR026546
 VERSION AR026546.1 GI:5937386
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

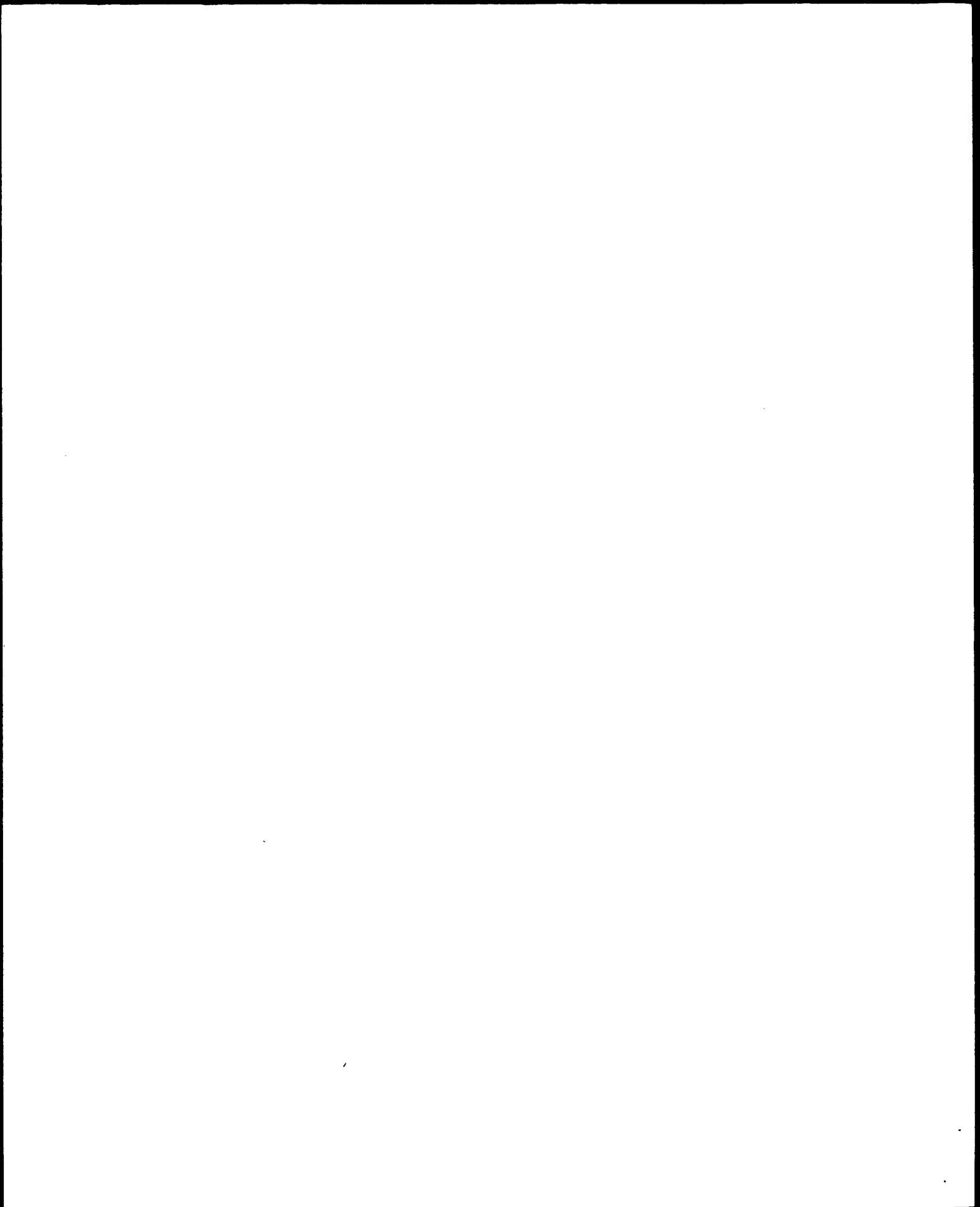
REFERENCE 1 (bases 1 to 24)
 AUTHORS Gray,D.M. and Clark,C.L.
 TITLE Method for selectively ranking sequences for antisense targeting
 JOURNAL Patent: US 5856103-A 9 05-JAN-1999;
 FEATURES Location/Qualifiers
 source 1..24
 /organism="unknown"

BASE COUNT 0 a 12 c 0 g 12 t
 ORIGIN

Query Match 100.0%; Score 13; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
 |||||
 Db 23 AGAGAGAGAGAGAGAG 6

Search completed: August 24, 2002, 21:54:45
 Job time: 22408 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 22:08:16 ; Search time 623.77 seconds
(without alignments)
49.545 Million cell updates/sec

Title: US-10-077-383-31

Perfect score: 18

Sequence: 1 agagagagagagagag 18

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_032802:*

1:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
7:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
8:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
10:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
11:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
16:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
17:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
18:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
19:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20:	/SID55/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21:	/SID55/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22:	/SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23:	/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24:	/SID55/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	100.0	18	20	AA91065
C 2	18	100.0	20	16	AA56904
C 3	18	100.0	21	18	AA86582
C 4	18	100.0	21	18	AA86583
C 5	18	100.0	22	13	AA33557
C 6	18	100.0	22	22	AA99703
C 7	18	100.0	23	13	AA33551
C 8	18	100.0	24	20	AA00524
C 9	18	100.0	24	20	AA00526

C 10	18	100.0	24	20	AA00525	Antisense oligonuc
C 11	18	100.0	24	20	AA00527	Antisense oligonuc
C 12	18	100.0	24	22	AAF57996	Nucleic acid tripl
C 13	18	100.0	24	22	AAF57997	Nucleic acid tripl
C 14	18	100.0	24	22	AAF57998	Nucleic acid tripl
C 15	18	100.0	24	22	AAF57999	Nucleic acid tripl
C 16	18	100.0	24	22	AAF58000	Nucleic acid tripl
C 17	18	100.0	24	22	AAF58001	Nucleic acid tripl
C 18	18	100.0	24	22	AAF58002	Nucleic acid tripl
C 19	18	100.0	24	22	AAF58003	Hybrid mRNA sequen
C 20	18	100.0	24	22	AAF58004	Hybrid mRNA sequen
C 21	18	100.0	24	22	AAF58005	Hybrid DNA sequen
C 22	18	100.0	26	17	AA87784	Hybrid DNA sequen
C 23	18	100.0	26	17	AA87785	Triple helix-formi
C 24	18	100.0	26	17	AA87786	Triple helix-formi
C 25	18	100.0	26	20	AA87787	T7 PCR primer
C 26	18	100.0	27	17	AA87788	Triplex-affinity D
C 27	18	100.0	27	22	AAH6006	Synthetic oligonuc
C 28	18	100.0	28	19	AAV5965	Oligonucleotide ta
C 29	18	100.0	28	19	AAV5966	Oligonucleotide ta
C 30	18	100.0	31	13	AAQ33520	Oligonucleotide ta
C 31	18	100.0	31	13	AAQ33521	Sequence of micros
C 32	18	100.0	32	13	AAQ33522	Microsatellite seq
C 33	18	100.0	32	13	AAQ33523	Sequence of micros
C 34	18	100.0	32	13	AAQ33524	Microsatellite seq
C 35	18	100.0	32	13	AAQ33525	Microsatellite seq
C 36	18	100.0	36	12	AAQ4028	N-D-Brdc oligonuc
C 37	18	100.0	36	13	AAQ33540	Microsatellite seq
C 38	18	100.0	38	22	AAH46872	Microsatellite seq
C 39	18	100.0	39	20	AAH46873	B. napus turgor ge
C 40	18	100.0	39	20	AAH46874	Maize SSR oligonuc
C 41	18	100.0	40	13	AAQ33618	Maize SSR oligonuc
C 42	18	100.0	40	18	AAH47455	Microsatellite seq
C 43	18	100.0	40	18	AAH47456	Foldback triplex f
C 44	18	100.0	41	15	AAQ78843	Foldback triplex f
C 45	18	100.0	41	19	AAV37415	HCWV Ab heavy chal
C 46	18	100.0	41	19	AAV37416	Oligonucleotide se

ALIGNMENTS

RESULT 1
ID AAX91065 standard; RNA; 18 BP.

AC AAX91065;

DT 15-NOV-1999 (first entry)

XX CAT gene target RNA fragment.

DE Phosphate internucleosidyl linkage; chirality: hybridization; racemic;

KW Binding affinity; ss.

OS Synthetic.

XX US9595597-A.

XX 21-SEP-1999.

XX 30-JUN-1997; 97US-0885126.

XX 21-NOV-1994; 94US-0343018.

XX 16-NOV-1993; 93US-0154013.

XX 30-JUN-1997; 97US-0885126.

XX (GENT-) GENTA INC.

XX Arnold LJ, Reynolds MA, Riley TA, Schwartz DA, Vaghefi MM;

XX WPI; 1999-539600/45.

XX Oligomers made using chirally pure nucleoside dimers, trimers, or

PT tetramers with enhanced binding affinities

XX Example 19; Column 41-42; 30pp; English.

XX The invention provides methods for preparing oligomers having
CC phosphonate internucleosidyl linkages of a preselected chirality which
CC hybridize to a target RNA sequence. The method of making comprises: (a)
CC synthesizing a nucleoside dimer, trimer, or tetramer with racemic
CC internucleosidyl phosphonate linkages; (b) purifying the racemic
CC nucleoside to a chirally pure nucleoside; and (c) sequentially linking at
CC least 2 of the chirally pure nucleosides to form a synthetic oligomer
CC that is enriched for phosphonate internucleosidyl linkages of a
CC preselected chirality and is complementary to an RNA target sequence. The
CC methods are useful for providing chirally enriched synthetic oligomers.
CC Rp chirally enriched synthetic oligomers have enhanced binding affinities
CC for RNA compared to oligomers with racemic all methylphosphonate
CC internucleosidyl linkages. Sequences AAX91054-75 represent oligomers
CC chemically synthesised using the method of the invention.

XX Sequence 18 BP; 0 A; 9 C; 0 G; 9 U; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18

DB 18 AGAGAGAGAGAGAGAG 1

RESULT 2

AAX56904/C
ID AAX56904 standard; RNA; 20 BP.

XX AAX56904;

XX 15-JUL-1999 (first entry)

DE W09526733 target strand RNA 9.

KW Cleavage; oligonucleoside; target; inter-strand orientation; inhibitor;
KW disease; treatment; internucleotidyl bond cleavage; primer; ss.

XX Synthetic.

XX W09526733-A1.

XX 12-OCT-1995.

XX 31-MAR-1995; 95WO-US03920.

XX 31-MAR-1994; 94US-0223355.

XX (GENT-) GENTA INC.

XX Arnold LJ, Dally WJ, Reynolds MA, Schwartz DA;

XX WPI; 1995-358439/46.

PT Oligo:nucleoside compounds for cleaving RNA - having a sequence that
PT is complementary to a target nucleic acid strand and a
PT non-complementary portion

XX Disclosure; Page 92; 109pp; English.

XX This invention describes a novel oligonucleoside compound for hybridising
CC to a target nucleic acid strand. The oligonucleoside comprises (a) an
CC oligonucleoside sequence that is complementary to a target region or
CC subregion of the target nucleic acid strand and (b) a portion that is
CC non-complementary to a target site in the target region or subregion such
CC that, when the oligonucleoside compound is hybridised to the target
CC strand, a base group at the site is oriented away from an inter-strand

CC orientation. The oligonucleoside and combinations are used for inhibiting
CC production of a selected protein in a cell by effecting cleavage at a
CC site in a target region of cellular RNA that codes for the selected
CC protein. They can be used for treating a condition in a mammal that is
CC caused by the production of a selected protein. The oligonucleosides are
CC target-mRNA-specific and can be used against mRNA specific to a
CC particular disease state. They are relatively harmless to non-targeted
CC nucleic acid. The non-complementary unit enhances internucleotidyl bond
CC cleavage.

XX Sequence 20 BP; 1 A; 9 C; 1 G; 9 U; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18

DB 19 AGAGAGAGAGAGAGAG 2

RESULT 3

AAT86582/C

ID AAT86582 standard; DNA; 21 BP.

XX AAT86582;

XX 25-MAR-1998 (first entry)

XX Phosphorothioate oligonucleotide #1.

XX Phosphorothioate oligonucleotide; dimeric phosphoramidite synthon;

KW thioester; DNA synthesis; antisense oligonucleotide; gene therapy;

XX ss.

XX Synthetic.

XX Key Location/Qualifiers

FT misc_difference 1..21

FT /*tag= a

FT /note= "Phosphorothioate linkages between alternate
FT nucleotides (1 and 2, 3 and 4 etc.)"

XX W09729116-A1.

XX 14-AUG-1997.

XX 06-FEB-1997; 97WO-GB00327.

XX 06-FEB-1996; 96GB-0002326.

XX (CRUA-) CRUACHEM LTD.

XX Rao MV, Reese CB;

XX WPI; 1997-415290/38.

PT Solid phase synthesis of phosphorothioate oligonucleotide(s) using
PT new dimeric synthon(s) - useful as anti-sense molecules for
PT inhibiting gene expression

XX Example 3; Page 20; 38pp; English.

XX The present sequence represents a phosphorothioate oligonucleotide which
CC was prepared by solid phase synthesis. The method comprises adding at
CC least one dimeric phosphoramidite synthon, optionally having a protected
CC thioester group in its internucleotide link, during the synthesis cycle.
CC These novel dimeric phosphoramidite synthons are used as antisense
CC molecules for inhibition of gene expression. The method gives increased
CC yields of the phosphorothioate oligonucleotide (since fewer cycles are
CC needed) and facilitates separation of impurities (greater difference
CC in size compared with use of monomeric synthons).

XX Sequence 21 BP; 0 A; 10 C; 0 G; 11 T; 0 other;
SQ Query Match 100.0%; Score 18; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agagagagagagagagag 18
|||||
Db 21 AGAGAGAGAGAGAGAG 4

RESULT 4
AAT86583/C
ID AAT86583 standard; DNA; 21 BP.
XX
AC AAT86583;
XX
DT 25-MAR-1998 (first entry)
XX
DE Phosphorothioate oligonucleotide #2.
XX
KW Phosphorothioate oligonucleotide; dimeric phosphoramidite synthon;
KW thioester; DNA synthesis; antisense oligonucleotide; gene therapy;
KW ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..21
FT /*tag= a
FT /note= "Phosphorothioate linkages between alternate
nucleotides (1 and 2, 3 and 4 etc.)"
XX
PW W09729116-A1.
XX
PD 14-AUG-1997.
XX
PF 06-FEB-1997; 97WO-GB00327.
XX
PR 06-FEB-1996; 96GB-0002326.
XX
PA (CRUA-) CRUCHEM LTD.
XX
PI Rao MV, Reese CB;
XX
DR WPI; 1997-415290/38.
XX
PT Solid phase synthesis of phosphorothioate oligonucleotide(s) using
PT new dimeric synthon(s) - useful as anti:sense molecules for
PT inhibiting gene expression
XX
PS Example 3; Page 25; 38pp; English.
XX
CC The present sequence represents a phosphorothioate oligonucleotide which
CC was prepared by solid phase synthesis. The method comprises adding at
CC least one dimeric phosphoramidite synthon, optionally having a protected
CC thioester group in its internucleotide link, during the synthesis cycle.
CC These novel dimeric phosphoramidite synthons are used as antisense
CC molecules for inhibition of gene expression. The method gives increased
CC yields of the phosphorothioate oligonucleotide (since fewer cycles are
CC needed) and facilitates separation of impurities (greater difference
CC in size compared with use of monomeric synthons).
XX
SQ Sequence 21 BP; 1 A; 10 C; 0 G; 10 T; 0 other;

Query Match 100.0%; Score 18; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agagagagagagagagag 18

Db 20 AGAGAGAGAGAGAGAG 3
|||||
RESULT 5
AAQ33557
ID AAQ33557 standard; DNA; 22 BP.
XX
AC AAQ33557;
XX
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone AGLA248.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN W09213102-A.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US00340.
XX
PR 15-JAN-1991; 91US-0642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX
PS Table 7; Page 151; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (TG)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved in the determination of economically important
CC traits esp. in cattle, to allow selective breeding.
XX
SQ See also AAQ33501-34437.
XX
SQ Sequence 22 BP; 11 A; 0 C; 10 G; 0 U; 1 other;

Query Match 100.0%; Score 18; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agagagagagagagagag 18
|||||
Db 3 agagagagagagagagag 20

RESULT 6
AAF99703/C
ID AAF99703 standard; DNA; 22 BP.
XX
AC AAF99703;
XX

DT 12-JUN-2001 (first entry)
 XX Immunostimulatory nucleic acid #819.
 DE
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX Synthetic.
 OS
 XX WO200122972-A2.
 PN
 XX 05-APR-2001.
 PD
 XX 25-SEP-2000; 2000WO-US26383.
 PF
 XX 25-SEP-1999; 99US-0156113.
 PR
 XX 27-SEP-1999; 99US-0156135.
 PR
 XX 23-AUG-2000; 2000US-0227436.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 PI Krieg AM, Schetter C, Vollmer J;
 XX
 XX WPI; 2001-273485/28.
 DR
 XX
 XX Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids -
 PT
 XX Claim 101; Page 56; 338pp; English.
 PS
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells.
 CC Note: the present sequence may have a phosphorothioate backbone.
 XX
 XX Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 other;
 SQ
 Query Match 100.0%; Score 18; DB 22; Length 22;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 agagagagagagagagag 18
 Db 22 AGAGAGAGAGAGAGAG 5
 |||||
 RESULT 7
 ID AAQ33511 standard; DNA; 23 BP.
 AC AAQ33511;
 XX
 XX 02-FEB-1993 (first entry)
 DT
 XX Sequence of microsatellite from clone AGLA209.
 DE
 XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 PR
 XX

OS Bos taurus.
 XX WO9213102-A.
 PN
 XX 06-AUG-1992.
 PD
 XX 15-JAN-1992; 92WO-US00340.
 PF
 XX 15-JAN-1991; 91US-0642342.
 PR
 XX (GENM-) GENMARK.
 PA
 XX Georges M, Massey JM;
 PI
 XX WPI; 1992-284684/34.
 DR
 XX Polymorphic bovine DNA markers - used in genetic identification,
 PT gene mapping, and selective breeding
 PT
 XX Table 7; Page 132; 517pp; English.
 PS
 XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a genomic library of bovine MboI DNA fragments of between
 CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
 CC One out of 50 clones cross-hybridised. Assuming independent
 CC distribution of microsatellites and MboI sites, the frequency of
 CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
 CC 000. The sequence information for ca. 230 such bovine microsatellites
 CC is summarised in the specification and indexed herein (see below).
 CC The sequences upstream and downstream of the microsatellite sequence
 CC were used to generate the required PCR primers for in vitro
 CC amplification of the corresp. microsatellite (using the program
 CC OPTIPRIM). The microsatellites may be used to identify individuals,
 CC for parentage testing, and in the genetic mapping of economic trait
 CC loci, or genes involved the determinism of economically important
 CC traits esp. in cattle, to allow selective breeding.
 CC See also AAQ33501-34437.
 XX
 SQ Sequence 23 BP; 12 A; 0 C; 11 G; 0 U; 0 other;
 Query Match 100.0%; Score 18; DB 13; Length 23;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 agagagagagagagagag 18
 Db 1 agagagagagagagagag 18
 |||||
 RESULT 8
 ID AAQ00524 standard; mRNA; 24 BP.
 XX
 XX AAQ00524;
 AC
 XX 30-MAR-1999 (first entry)
 DT
 XX Target sequence #2 for antisense oligonucleotides.
 DE
 XX Target; antisense; selective rank; inhibition; ranking; stability;
 KW interaction; ss.
 KW
 XX Synthetic.
 OS
 XX US5856103-A.
 PN
 XX 05-JAN-1999.
 PD
 XX 03-MAR-1997; 97US-0808474.
 PF
 XX 03-MAR-1997; 97US-0808474.
 PR
 XX 07-OCT-1994; 94US-0320507.
 PR

XX (TEXA) UNIV TEXAS.
 XX Clark CL, Gray DM;
 XX WPI; 1999-105098/09.
 XX
 XX Selectively ranking nucleic acid molecules, for inhibitory
 PT efficiency - comprises determining the fraction a set of
 PT nearest-neighbour nucleic acid base pair types in a target sequence
 PT zone, substituting nearest-neighbour nucleic acid base pair
 PT fractions to determine the fractions and multiplying
 XX
 XX Disclosure; Column 13-14; 72pp; English.
 XX
 XX This sequence represents a target mRNA for the generation of antisense
 CC oligonucleotides (ASO) in a method of selectively ranking nucleic acid
 CC molecules for inhibitory efficiency. The method comprises:
 CC (a) determining the fraction of each of a set of 13 nearest-neighbour
 CC nucleic acid base pair types in a target sequence zone RNA:ASO-DNA hybrid
 CC nucleic acid sequence; (b) substituting nearest-neighbour nucleic acid
 CC base pair fractions into formulas to determine the fractions of each of
 CC a series of 13 nearest-neighbour nucleic acid base pair types to provide
 CC determined fractions; and (c) multiplying the fractions of the 13
 CC nearest-neighbour nucleic acid base pair types by a stability ranking
 CC to the nucleic acid antisense sequence; where the results are ordered
 CC to produce a ranking. The process is used to rank nucleic acid sequences
 CC based on the stability of nucleic acid oligomer binding interactions to
 CC select sequence zones for antisense targeting.
 XX
 XX Sequence 24 BP; 12 A; 12 C; 12 G; 0 U; 0 other;
 SQ

Query Match 100.08; Score 18; DB 20; Length 24;
 Best Local Similarity 100.08; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
 |||||
 Db 1 agagagagagagagagag 18
 |||||

RESULT 9
 AAX00526/c
 ID AAX00526 standard; mRNA; 24 BP.
 XX
 XX AAX00526;
 XX
 XX 30-MAR-1999 (first entry)
 XX
 XX Poly-pyrimidine target sequence for antisense oligonucleotides.
 DE Target; antisense; selective rank; inhibition; ranking; stability;
 KW interaction; ss.
 KW
 XX Synthetic.
 XX
 XX US5856103-A.
 PN
 XX 05-JAN-1999.
 PD
 XX 03-MAR-1997; 97US-0808474.
 XX
 XX 03-MAR-1997; 97US-0808474.
 PR
 XX 07-OCT-1994; 94US-0320507.
 PR
 XX (TEXA) UNIV TEXAS.
 PA
 XX Clark CL, Gray DM;
 PI
 XX WPI; 1999-105098/09.
 XX
 XX Selectively ranking nucleic acid molecules, for inhibitory

PT efficiency - comprises determining the fraction a set of
 PT nearest-neighbour nucleic acid base pair types in a target sequence
 PT zone, substituting nearest-neighbour nucleic acid base pair
 PT fractions to determine the fractions and multiplying
 XX
 XX Disclosure; Column 13-14; 72pp; English.
 XX
 XX This sequence represents a target mRNA for the generation of antisense
 CC oligonucleotides (ASO) in a method of selectively ranking nucleic acid
 CC molecules for inhibitory efficiency. The method comprises:
 CC (a) determining the fraction of each of a set of 13 nearest-neighbour
 CC nucleic acid base pair types in a target sequence zone RNA:ASO-DNA hybrid
 CC nucleic acid sequence; (b) substituting nearest-neighbour nucleic acid
 CC base pair fractions into formulas to determine the fractions of each of
 CC a series of 13 nearest-neighbour nucleic acid base pair types to provide
 CC determined fractions; and (c) multiplying the fractions of the 13
 CC nearest-neighbour nucleic acid base pair types by a stability ranking
 CC to the nucleic acid antisense sequence; where the results are ordered
 CC to produce a ranking. The process is used to rank nucleic acid sequences
 CC based on the stability of nucleic acid oligomer binding interactions to
 CC select sequence zones for antisense targeting.
 XX
 XX Sequence 24 BP; 0 A; 12 C; 12 G; 12 U; 0 other;
 SQ

Query Match 100.08; Score 18; DB 20; Length 24;
 Best Local Similarity 100.08; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
 |||||
 Db 23 AGAGAGAGAGAGAGAG 6

RESULT 10
 AAX00525/c
 ID AAX00525 standard; DNA; 24 BP.
 XX
 XX AAX00525;
 XX
 XX 30-MAR-1999 (first entry)
 XX
 XX Antisense oligonucleotide for poly-purine target sequence.
 DE Target; antisense; selective rank; inhibition; ranking; stability;
 KW interaction; ss.
 KW
 XX Synthetic.
 XX
 XX US5856103-A.
 PN
 XX 05-JAN-1999.
 PD
 XX 03-MAR-1997; 97US-0808474.
 XX
 XX 03-MAR-1997; 97US-0808474.
 PR
 XX 07-OCT-1994; 94US-0320507.
 PR
 XX (TEXA) UNIV TEXAS.
 PA
 XX Clark CL, Gray DM;
 PI
 XX WPI; 1999-105098/09.
 XX
 XX Selectively ranking nucleic acid molecules, for inhibitory
 PT efficiency - comprises determining the fraction a set of
 PT nearest-neighbour nucleic acid base pair types in a target sequence
 PT zone, substituting nearest-neighbour nucleic acid base pair
 PT fractions to determine the fractions and multiplying
 XX
 XX Disclosure; Column 13-14; 72pp; English.
 XX
 XX This oligonucleotide represents an antisense oligonucleotides (ASO)

CC targeted to a poly-purine mRNA sequence generated by a method of
 CC selectively ranking nucleic acid molecules for inhibitory efficiency.
 CC The method comprises: (a) determining the fraction of each of a set of
 CC 13 nearest-neighbour nucleic acid base pair types in a target sequence
 CC zone RNA:ASO-DNA hybrid nucleic acid sequence; (b) substituting
 CC nearest-neighbour nucleic acid base pair fractions into formulas to
 CC determine the fractions of each of a series of 13 nearest-neighbour
 CC nucleic acid base pair types to provide determined fractions; and
 CC (c) multiplying the fractions of the 13 nearest-neighbour nucleic acid
 CC base pair types by a stability ranking to the nucleic acid antisense
 CC sequence; where the results are ordered to produce a ranking.
 CC The process is used to rank nucleic acid sequences based on the
 CC stability of nucleic acid oligomer binding interactions to select
 CC sequence zones for antisense targeting.
 XX Sequence 24 BP; 0 A; 12 C; 0 G; 12 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 agagagagagagagagag 18
 Db 24 AGAGAGAGAGAGAGAG 7
 |||||

RESULT 11
 AAX00527
 ID AAX00527 standard; DNA; 24 BP.
 XX AC AAX00527;
 XX 30-MAR-1999 (first entry)
 DE Antisense oligonucleotide for poly-pyrimidine target sequence.
 DE Target: antisense; selective rank; inhibition; ranking; stability;
 KW interaction; ss.
 XX Synthetic.
 XX US5856103-A.
 XX 05-JAN-1999.
 XX 03-MAR-1997; 97US-0808474.
 PR 03-MAR-1997; 97US-0808474.
 PR 07-OCT-1994; 94US-0320507.
 XX (TEXA) UNIV TEXAS.
 PA Clark CL, Gray DM;
 PI WPI; 1999-105098/09.
 DR Selectively ranking nucleic acid molecules, for inhibitory
 PT efficiency - comprises determining the fraction of a set of
 PT nearest-neighbour nucleic acid base pair types in a target
 PT zone, substituting nearest-neighbour nucleic acid base pair
 PT fractions to determine the fractions and multiplying
 XX Disclosure; Column 13-14; 72pp; English.
 XX This oligonucleotide represents an antisense oligonucleotides (ASO)
 CC targeted to a poly-pyrimidine mRNA sequence generated by a method of
 CC selectively ranking nucleic acid molecules for inhibitory efficiency.
 CC The method comprises: (a) determining the fraction of each of a set of
 CC 13 nearest-neighbour nucleic acid base pair types in a target sequence
 CC zone RNA:ASO-DNA hybrid nucleic acid sequence; (b) substituting
 CC nearest-neighbour nucleic acid base pair fractions into formulas to
 CC determine the fractions of each of a series of 13 nearest-neighbour

CC nucleic acid base pair types to provide determined fractions; and
 CC (c) multiplying the fractions of the 13 nearest-neighbour nucleic acid
 CC base pair types by a stability ranking to the nucleic acid antisense
 CC sequence; where the results are ordered to produce a ranking.
 CC The process is used to rank nucleic acid sequences based on the
 CC stability of nucleic acid oligomer binding interactions to select
 CC sequence zones for antisense targeting.
 XX Sequence 24 BP; 12 A; 0 C; 12 G; 0 U; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
 Db 2 agagagagagagagagag 19
 |||||

RESULT 12
 AAF57996/C
 ID AAF57996 standard; DNA; 24 BP.
 XX AC AAF57996;
 XX 26-APR-2001 (first entry)
 DE Nucleic acid triplex DNA sequence #1.
 DE Hoogsteen-paired duplex; Watson-Crick pairing; triplex;
 KW antisense therapy; gene expression control; transcription; ss.
 XX Synthetic.
 XX WO200105937-A2.
 XX 25-JAN-2001.
 XX 20-JUL-2000; 2000WO-US19783.
 XX 20-JUL-1999; 98US-0357424.
 PR 19-JAN-2000; 2000US-0487130.
 XX (TEXA) UNIV TEXAS.
 PA Gray DM, Hashem GM;
 PI WPI; 2001-159523/16.
 DR Generating nucleic acid molecule comprising Hoogsteen-paired
 PT RNAsteriskDNA pyrimidinesteriskpurine duplex for use as an antisense
 PT molecule, by heating a triplex to dissociate a Watson-Crick paired
 PT pyrimidine strand -
 XX Example 1; Page 9; 23pp; English.
 XX The present invention describes a method for producing a nucleic acid
 CC molecule comprising a Hoogsteen-paired RNA:DNA duplex capable of being
 CC used as an antisense molecule and capable of recognising an RNA sequence
 CC to form a triplex. This involves Watson-Crick pairing. This is useful in
 CC antisense therapy, as it controls gene expression by causing in
 CC transcription to be prevented. The present sequence is an example of a
 CC triplex sequence used in the methods of the invention.
 XX Sequence 24 BP; 0 A; 12 C; 0 G; 12 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 agagagagagagagagag 18

Db 24 AGAGAGAGAGAGAGAG 7
|||||

RESULT 13

AAF57997
ID AAF57997 standard; DNA; 24 BP.

AC AAF57997;

XX 26-APR-2001 (first entry)

XX Nucleic acid triplex DNA sequence #2.

XX Hoogsteen-paired duplex; Watson-Crick pairing; triplex;

KW antisense therapy; gene expression control; transcription; ss.

XX Synthetic.

XX WO200105937-A2.

XX 25-JAN-2001.

XX 20-JUL-2000; 2000WO-US19783.

XX 20-JUL-1999; 99US-0357424.

PR 19-JAN-2000; 2000US-0487130.

XX (TEXA) UNIV TEXAS.

XX Gray DM, Hashem GM;

XX WPI; 2001-159523/16.

XX Generating nucleic acid molecule comprising Hoogsteen-paired

PT RNAsteriskDNA pyrimidinesteriskpurine duplex for use as an antisense

PT molecule, by heating a triplex to dissociate a Watson-Crick paired

PT pyrimidine strand -

XX Example 1; Page 9; 23pp; English.

XX The present invention describes a method for producing a nucleic acid
CC molecule comprising a Hoogsteen-paired RNA-DNA duplex capable of being
CC used as an antisense molecule and capable of recognising an RNA sequence
CC to form a triplex. This involves Watson-Crick pairing. This is useful in
CC antisense therapy, as it controls gene expression by causing
CC transcription to be prevented. The present sequence is an example of a
CC triplex sequence used in the methods of the invention.

XX Sequence 24 BP; 12 A; 0 C; 12 G; 0 U; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 24;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18

Db 1 agagagagagagagagag 18

RESULT 14

AAF57998/c
ID AAF57998 standard; DNA; 24 BP.

AC AAF57998;

XX 26-APR-2001 (first entry)

XX Nucleic acid triplex DNA sequence #3.

XX Hoogsteen-paired duplex; Watson-Crick pairing; triplex;

KW antisense therapy; gene expression control; transcription; ss.

XX Synthetic.
XX WO200105937-A2.
XX 25-JAN-2001.
XX 20-JUL-2000; 2000WO-US19783.
XX 20-JUL-1999; 99US-0357424.
PR 19-JAN-2000; 2000US-0487130.
XX (TEXA) UNIV TEXAS.
XX Gray DM, Hashem GM;
XX WPI; 2001-159523/16.
XX Generating nucleic acid molecule comprising Hoogsteen-paired
PT RNAsteriskDNA pyrimidinesteriskpurine duplex for use as an antisense
PT molecule, by heating a triplex to dissociate a Watson-Crick paired
PT pyrimidine strand -
XX Example 1; Page 9; 23pp; English.
XX The present invention describes a method for producing a nucleic acid
CC molecule comprising a Hoogsteen-paired RNA-DNA duplex capable of being
CC used as an antisense molecule and capable of recognising an RNA sequence
CC to form a triplex. This involves Watson-Crick pairing. This is useful in
CC antisense therapy, as it controls gene expression by causing
CC transcription to be prevented. The present sequence is an example of a
CC triplex sequence used in the methods of the invention.

XX Sequence 24 BP; 0 A; 12 C; 0 G; 12 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18

Db 24 AGAGAGAGAGAGAGAG 7

RESULT 15

AAF57999/c

ID AAF57999 standard; RNA; 24 BP.

XX AAF57999;

XX 26-APR-2001 (first entry)

XX Nucleic acid triplex RNA sequence #1.

XX Hoogsteen-paired duplex; Watson-Crick pairing; triplex;

KW antisense therapy; gene expression control; transcription; ss.

XX Synthetic.

XX WO200105937-A2.

XX 25-JAN-2001.

XX 20-JUL-2000; 2000WO-US19783.

XX 20-JUL-1999; 99US-0357424.

PR 19-JAN-2000; 2000US-0487130.

XX (TEXA) UNIV TEXAS.

XX Gray DM, Hashem GM;

DR WPI; 2001-159523/16.
 XX
 PT Generating nucleic acid molecule comprising Hoogsteen-paired
 PT RNasesteriskDNA pyrimidineesteriskpurine duplex for use as an antisense
 PT molecule, by heating a triplex to dissociate a Watson-Crick paired
 XX pyrimidine strand -
 PS
 XX Claim 14; Page 17; 23pp; English.
 CC
 CC The present invention describes a method for producing a nucleic acid
 CC molecule comprising a Hoogsteen-paired RNA:DNA duplex capable of being
 CC used as an antisense molecule and capable of recognising an RNA sequence
 CC to form a triplex. This involves Watson-Crick pairing. This is useful in
 CC antisense therapy, as it controls gene expression by causing
 CC transcription to be prevented. The present sequence is an example of a
 CC triplex sequence used in the methods of the invention.
 XX
 SQ Sequence 24 BP; 0 A; 12 C; 0 G; 12 U; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 agagagagagagagagag 18
 Db 24 AGAGAGAGAGAGAGAGAG 7

Search completed: August 24, 2002, 22:08:17
 Job time: 8850 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 21:57:39 ; Search time 159.68 Seconds
(without alignments)
27.689 Million cell updates/sec

Title: US-10-077-383-31

Perfect score: 18

Sequence: 1 agagagagagagagagag 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2.6/ptodata/2/ina/5A.COMB.seq.*
- 2: /cgn2.6/ptodata/2/ina/5B.COMB.seq.*
- 3: /cgn2.6/ptodata/2/ina/6A.COMB.seq.*
- 4: /cgn2.6/ptodata/2/ina/6B.COMB.seq.*
- 5: /cgn2.6/ptodata/2/ina/6C.COMB.seq.*
- 6: /cgn2.6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	100.0	18	2	US-08-885-126-12
C 2	18	100.0	18	4	US-08-700-530-4
C 3	18	100.0	20	1	US-08-004-552-1
C 4	18	100.0	20	2	US-08-223-355-23
C 5	18	100.0	20	2	US-08-863-639A-72
C 6	18	100.0	20	2	US-08-863-639A-93
C 7	18	100.0	24	2	US-08-808-474A-8
C 8	18	100.0	24	2	US-08-808-474A-9
C 9	18	100.0	24	2	US-08-808-474A-10
C 10	18	100.0	24	2	US-08-808-474A-11
C 11	18	100.0	24	4	US-09-235-614-8
C 12	18	100.0	24	4	US-09-235-614-9
C 13	18	100.0	24	4	US-09-235-614-10
C 14	18	100.0	24	4	US-09-235-614-11
C 15	18	100.0	26	4	US-08-860-038-19
C 16	18	100.0	26	4	US-09-580-923-19
C 17	18	100.0	27	1	US-08-004-552-2
C 18	18	100.0	28	3	US-08-946-138-1
C 19	18	100.0	28	4	US-09-225-652-1
C 20	18	100.0	32	1	US-08-469-802B-28
C 21	18	100.0	32	2	US-08-267-803B-46
C 22	18	100.0	36	4	US-09-387-300-31
C 23	18	100.0	43	1	US-08-473-096-1
C 24	18	100.0	43	1	US-08-473-096-2
C 25	18	100.0	43	1	US-08-473-096-3
C 26	18	100.0	43	1	US-08-473-096-4
C 27	18	100.0	43	1	US-08-473-096-5

c 28	18	100.0	43	1	US-08-473-096-6
c 29	18	100.0	43	1	US-08-473-096-7
c 30	18	100.0	43	1	US-08-473-096-8
c 31	18	100.0	43	1	US-08-473-096-9
c 32	18	100.0	43	1	US-08-473-096-11
c 33	18	100.0	43	1	US-08-473-096-12
c 34	18	100.0	43	1	US-08-473-096-13
c 35	18	100.0	43	1	US-08-473-096-14
c 36	18	100.0	43	4	US-09-387-300-35
c 37	18	100.0	44	1	US-08-222-177A-385
c 38	18	100.0	44	4	US-09-240-918-79
c 39	18	100.0	45	1	US-07-912-900-10
c 40	18	100.0	45	1	US-08-285-309-10
c 41	18	100.0	45	1	US-08-313-075A-6
c 42	18	100.0	45	2	US-08-379-556A-11
c 43	18	100.0	45	2	US-08-379-482A-1
c 44	18	100.0	45	2	US-08-502-046-10
c 45	18	100.0	46	1	US-08-249-112-5

ALIGNMENTS

RESULT 1

US-08-885-126-12/c
; Sequence 12, Application US/08885126A

; Patent No. 5955597

; GENERAL INFORMATION:

; APPLICANT: Arnold, Lyle J.

; APPLICANT: Riley, Timothy A.

; APPLICANT: Reynolds, Mark A.

; APPLICANT: Schwartz, David A.

; TITLE OF INVENTION: CHIRALLY ENRICHED SYNTHETIC PHOSPHATE

; TITLE OF INVENTION: OLIGOMERS

; FILE REFERENCE: GENTA.020FW2

; CURRENT APPLICATION NUMBER: US/08/885,126A

; CURRENT FILING DATE: 1997-06-30

; EARLIER APPLICATION NUMBER: 08/343,018

; EARLIER FILING DATE: 1994-11-21

; EARLIER APPLICATION NUMBER: 08/154,013

; EARLIER FILING DATE: 1993-11-16

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: Fastseq for Windows Version 3.0

; SEQ ID NO 12

; LENGTH: 18

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized oligomer

US-08-885-126-12

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagag 18

Db 18 AGAGAGAGAGAGAGAG 1

RESULT 2

US-08-700-530-4/c

; Sequence 4, Application US/08700530

; Patent No. 6316186

; GENERAL INFORMATION:

; APPLICANT: EKINS, Roger P

; TITLE OF INVENTION: Binding assay using binding agents with tail groups

; FILE REFERENCE: 0380-P0180US0

; CURRENT APPLICATION NUMBER: US/08/700,530

; CURRENT FILING DATE: 1996-10-23

; PRIOR APPLICATION NUMBER: PCT/GB95/00521

; PRIOR FILING DATE: 1995-03-10

; PRIOR APPLICATION NUMBER: GB 9404709.9
 ; PRIOR FILING DATE: 1994-03-11
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 4 \
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: Oligonucleotide
 US-08-700-530-4

Query Match 100.0%; Score 18; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
 Db 18 AGAGAGAGAGAGAGAG 1

RESULT 3
 US-08-004-552-1/c
 ; Sequence 1, Application US/08004552
 ; Patent No. 5482836
 ; GENERAL INFORMATION:
 ; APPLICANT: Cantor, Charles R.
 ; APPLICANT: Ito, Takashi
 ; APPLICANT: Smith, Cassandra L.
 ; TITLE OF INVENTION: DNA PURIFICATION BY TRIPLEX-AFFINITY
 ; TITLE OF INVENTION: CAPTURE AND AFFINITY CAPTURE ELECTROPHORESIS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Karen S. Smith
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: CA 94111

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 19930114
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, Karen S.
 ; REGISTRATION NUMBER: 31,426
 ; REFERENCE/DOCKET NUMBER: A-57666/KSS
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: 1..20
 ; OTHER INFORMATION: /note= "BPC-20 oligonucleotide,
 ; OTHER INFORMATION: biotinylated at 5'-end."
 US-08-004-552-1

Query Match 100.0%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
 Db 19 AGAGAGAGAGAGAGAG 2

RESULT 4
 US-08-223-355-23/c
 ; Sequence 23, Application US/08223355
 ; Patent No. 5854410
 ; GENERAL INFORMATION:
 ; APPLICANT: Arnold Jr., Lyle J.
 ; APPLICANT: Reynolds, Mark A.
 ; APPLICANT: Schwartz, David A.
 ; APPLICANT: Dally, William J.
 ; TITLE OF INVENTION: Oligonucleoside Cleavage Compounds and
 ; TITLE OF INVENTION: Therapies
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 611 W. Sixth St.
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90017

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/223,355
 ; FILING DATE: 31-MAR-1994
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meier, Paul H.
 ; REGISTRATION NUMBER: 32,274
 ; REFERENCE/DOCKET NUMBER: 200/069
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 213/489-1600
 ; TELEFAX: 213/955-0440
 ; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; HYPOTHETICAL: Yes
 ; ANTI-SENSE: NO
 ; FEATURE:
 ; NAME/KEY: R183
 ; OTHER INFORMATION: target strand
 US-08-223-355-23

Query Match 100.0%; Score 18; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
 Db 19 AGAGAGAGAGAGAGAG 2

RESULT 5
 US-08-863-639A-72
 ; Sequence 72, Application US/08863639A
 ; Patent No. 5981185
 ; GENERAL INFORMATION:

us-10-077-383-31.rni

Mon Aug 26 10:18:14 2002

```

;
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-72

Query Match 100.0%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
Db 1 AGAGAGAGAGAGAGAG 18

RESULT 6
US-08-863-639A-93/C
; Sequence 93, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A

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;
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-93

Query Match 100.0%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
Db 20 AGAGAGAGAGAGAGAGAG 3

RESULT 7
US-08-808-474A-8
; Sequence 8, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; TITLE OF INVENTION: FOR ANTISENSE TARGETING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,474A
; FILING DATE: 03-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTDAI-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 740-8000
; TELEFAX: (214) 740-8800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-808-474A-8

Query Match 100.0%; Score 18; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 agagagagagagagagag 18
Db 1 AGAGAGAGAGAGAGAG 18

RESULT 8
US-08-808-474A-9/c
; Sequence 9, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; TITLE OF INVENTION: FOR ANTISENSE TARGETING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTDAL:001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 740-8800
; TELEFAX: (214) 740-8800
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-808-474A-9

Query Match 100.0%; Score 18; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
Db 23 AGAGAGAGAGAGAGAG 6

RESULT 9
US-08-808-474A-10/c
; Sequence 10, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; TITLE OF INVENTION: FOR ANTISENSE TARGETING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTDAL:001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 740-8800
; TELEFAX: (214) 740-8800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-808-474A-10

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Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
Db 23 AGAGAGAGAGAGAGAG 6

RESULT 10
US-08-808-474A-11
; Sequence 11, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; TITLE OF INVENTION: FOR ANTISENSE TARGETING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTDAL:001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 740-8800
; TELEFAX: (214) 740-8800
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-808-474A-11

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Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGAGAGAGAGAGAGAG 18

RESULT 11
US-09-235-614-8
; Sequence 8, Application US/09235614
; Patent No. 6183966
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: CLARK, CHRISTOPHER L.
; TITLE OF INVENTION: AN APPARATUS AND METHOD FOR SELECTIVELY RANKING
; TITLE OF INVENTION: SEQUENCES FOR ANTISENSE TARGETING
; FILE REFERENCE: 91556/66384
; CURRENT APPLICATION NUMBER: US/09/235,614
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/808,474
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 08/320,507
; PRIOR FILING DATE: 1994-10-07
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid mRNA
US-09-235-614-8

Query Match 100.0%; Score 18; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
|||||
DB 1 agagagagagagagagag 18

RESULT 12
US-09-235-614-9/c
; Sequence 9, Application US/09235614
; Patent No. 6183966
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: CLARK, CHRISTOPHER L.
; TITLE OF INVENTION: AN APPARATUS AND METHOD FOR SELECTIVELY RANKING
; TITLE OF INVENTION: SEQUENCES FOR ANTISENSE TARGETING
; FILE REFERENCE: 91556/66384
; CURRENT APPLICATION NUMBER: US/09/235,614
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/808,474
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 08/320,507
; PRIOR FILING DATE: 1994-10-07
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA
US-09-235-614-9

Query Match 100.0%; Score 18; DB 4; Length 24;

Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
|||||
DB 24 AGAGAGAGAGAGAGAG 7

RESULT 13
US-09-235-614-10/c
; Sequence 10, Application US/09235614
; Patent No. 6183966
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: CLARK, CHRISTOPHER L.
; TITLE OF INVENTION: AN APPARATUS AND METHOD FOR SELECTIVELY RANKING
; TITLE OF INVENTION: SEQUENCES FOR ANTISENSE TARGETING
; FILE REFERENCE: 91556/66384
; CURRENT APPLICATION NUMBER: US/09/235,614
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/808,474
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 08/320,507
; PRIOR FILING DATE: 1994-10-07
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid mRNA
US-09-235-614-10

Query Match 100.0%; Score 18; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
|||||
DB 23 AGAGAGAGAGAGAGAG 6

RESULT 14
US-09-235-614-11
; Sequence 11, Application US/09235614
; Patent No. 6183966
; GENERAL INFORMATION:
; APPLICANT: GRAY, DONALD M.
; APPLICANT: CLARK, CHRISTOPHER L.
; TITLE OF INVENTION: AN APPARATUS AND METHOD FOR SELECTIVELY RANKING
; TITLE OF INVENTION: SEQUENCES FOR ANTISENSE TARGETING
; FILE REFERENCE: 91556/66384
; CURRENT APPLICATION NUMBER: US/09/235,614
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/808,474
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 08/320,507
; PRIOR FILING DATE: 1994-10-07
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA
US-09-235-614-11

Query Match 100.0%; Score 18; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.2;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
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Db 2 agagagagagagagagag 19

RESULT 15

US-08-860-038-19/c
; Sequence 19, Application US/08860038
; Patent No. 6287762
; GENERAL INFORMATION:
; APPLICANT: CROUZET, Joel
; APPLICANT: SCHERMAN, Daniel
; APPLICANT: WILS, Pierre
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
; TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,038
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/15162
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/01468
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST94090-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-19

Query Match 100.0%; Score 18; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 2 AGAGAGAGAGAGAGAGAG 9

Search completed: August 24, 2002, 21:57:39
Job time: 21597 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 21:19:25 ; Search time 4810.92 seconds
(without alignments)
50.499 Million cell updates/sec

Title: US-10-077-383-31

Perfect score: 18
Sequence: 1 ageagagagagagag 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
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12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vit:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 3	18	100.0	19	12	A2983014
C 4	18	100.0	20	12	A2433566
C 5	18	100.0	20	12	A2492997
C 6	18	100.0	20	12	A2770557
C 7	18	100.0	21	12	A2394897
C 8	18	100.0	21	12	A2589098
C 9	18	100.0	21	12	A2627978
C 10	18	100.0	22	12	A2464354
C 11	18	100.0	22	12	A2633751
C 12	18	100.0	23	12	A2430288
C 13	18	100.0	23	12	A2822888
C 14	18	100.0	23	12	A2973926
C 15	18	100.0	25	12	A2389918
C 16	18	100.0	25	12	A2510124
C 17	18	100.0	25	12	A2659095

C 18	100.0	25	12	A2664804
C 19	100.0	26	12	A2342914
C 20	100.0	26	12	A2579594
C 21	100.0	26	12	A2641486
C 22	100.0	26	12	A2666145
C 23	100.0	26	12	A2771239
C 24	100.0	26	12	A2803946
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C 26	100.0	26	12	A2939813
C 27	100.0	27	12	A2632991
C 28	100.0	27	12	A2655531
C 29	100.0	27	12	A2776487
C 30	100.0	27	12	A2873739
C 31	100.0	28	12	A2462549
C 32	100.0	28	12	A2860136
C 33	100.0	28	12	A2943199
C 34	100.0	29	12	A2455946
C 35	100.0	29	12	A2804183
C 36	100.0	30	12	A2610578
C 37	100.0	31	12	A2641732
C 38	100.0	31	12	A2869598
C 39	100.0	32	12	A2345558
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ALIGNMENTS

RESULT 1
AZ489586/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

AZ489586 19 bp DNA linear GSS 05-OCT-2000
Clone UUGC1M0322C12 F, DNA sequence.

AZ489586

AZ489586.1 GI:10659481

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0322 row: C column: 12

Seq primer: GCTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0322C12"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii4732114|db|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 10 c 9 t
 ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 18 AGAGAGAGAGAGAGAG 1

RESULT 2
 AZ510952/c

LOCUS 19 bp DNA linear GSS 05-OCT-2000
 DEFINITION IM0355G15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0355G15 R, DNA sequence.

ACCESSION AZ510952
 VERSION AZ510952.1 GI:10692268

KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5605
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 Seq primer: CACAGAGAACAGCTATGACC
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 High quality sequence stop: 19.

FEATURES source
 1..19 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0355G15"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii4732114|db|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 9 c 0 g 10 t
 ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18
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Db 19 AGAGAGAGAGAGAGAG 2

RESULT 3
 AZ983014/c

LOCUS 19 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0264H02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0264H02 F, DNA sequence.

ACCESSION AZ983014
 VERSION AZ983014.1 GI:13854241

KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0264 row: H column: 02
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES source
 1..19 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"

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/clones="UUGC2M0264H02"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g147321141gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      9 c      1 g      9 t
ORIGIN

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Query Match      100.0%; Score 18; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 19 AGACAGAGAGAGAGAG 2

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RESULT 4
AZ433566/c
LOCUS      20 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION 1M0219C02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION  AZ433566
VERSION     AZ433566.1 GI:10557579
KEYWORDS   GSS.
SOURCE      house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0219 row: C column: 02
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES   Location/Qualifiers
            1..20
            /organism="Mus musculus"
            /strain="C57BL/6J"

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/db_xref="taxon:10090"
/clones="UUGC1M0219C02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g147321141gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      10 c      0 g      10 t
ORIGIN

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Query Match      100.0%; Score 18; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 agagagagagagagag 18
    |||||
Db 20 AGAGAGAGAGAGAGAG 3

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RESULT 5
AZ492997/c
LOCUS      20 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION 1M0327K24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION  AZ492997
VERSION     AZ492997.1 GI:10666247
KEYWORDS   GSS.
SOURCE      house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0327 row: K column: 24
            Seq primer: CGTTGTAACACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES   Location/Qualifiers
            1..20
            /organism="Mus musculus"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0327K24"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii14732114|gbi|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      0 g      10 t
ORIGIN
Query Match      100.0%; Score 18; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagag 18
    |||||
Db 19 AGAGAGAGAGAGAGAG 2

RESULT 6
AZ770557/c
LOCUS      20 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION      LM0572N08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0572N08 F, DNA sequence.
ACCESSION      AZ770557
VERSION      AZ770557.1 GI:12891863
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0572 row: N column: 08
Seq primer: CGTTGTAAACGAGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0572N08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii14732114|gbi|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      10 c      0 g      10 t
ORIGIN
Query Match      100.0%; Score 18; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagag 18
    |||||
Db 19 AGAGAGAGAGAGAGAG 2

RESULT 7
AZ394897/c
LOCUS      21 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION      IM0158H11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0158H11 R, DNA sequence.
ACCESSION      AZ394897
VERSION      AZ394897.1 GI:10509969
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0158 row: H column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

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source
1. 21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0158H11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gii473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      10 c      0 g      11 t
ORIGIN

Query Match      100.0%; Score 18; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagag 18
    |||||
Db 21 AGAGAGAGAGAGAGAG 4

RESULT 8
A2589098
LOCUS
DEFINITION
1M0397B19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0397B19 R, DNA sequence.
ACCESSION
A2589098
VERSION
A2589098.1 GI:11711288
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,F., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0397 row: B column: 19
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0397B19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gii473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      11 a      0 c      10 g      0 t
ORIGIN

Query Match      100.0%; Score 18; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagag 18
    |||||
Db 1 AGAGAGAGAGAGAGAG 18

RESULT 9
A2527978/c
LOCUS
DEFINITION
1M0476L04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0476L04 F, DNA sequence.
ACCESSION
A2527978
VERSION
A2527978.1 GI:11750168
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,F., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: L column: 04
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends

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High quality sequence stop: 21.

FEATURES

Location/Qualifiers
1. .21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0476104"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

0 a 10 c 0 g 11 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18

Db 21 AGAGAGAGAGAGAGAG 4

RESULT 10

AZ464354/c

LOCUS

DEFINITION

1M0273M1R Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0273M1 R, DNA sequence.

ACCESSION

AZ464354

VERSION

AZ464354.1 GI:10622479

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0273 row: M column: 11

Seq primer: CACACAGGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

Location/Qualifiers
1. .22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0273M1"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1 a 10 c 0 g 11 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 22;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agagagagagagagagag 18

Db 21 AGAGAGAGAGAGAGAG 4

RESULT 11

AZ633751/c

LOCUS

DEFINITION

1M0489I1F Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0489I1 F, DNA sequence.

ACCESSION

AZ633751

VERSION

AZ633751.1 GI:11755941

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0489 row: I column: 11

Seq primer: CGTTGTAAACAGCGGCAAT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M048911"
/cclone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1147321141gblAFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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BASE COUNT 0 a 11 c 0 g 11 t
 ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagag 18
 |||||

Db 21 AGAGAGAGAGAGAGAG 4

RESULT 12
 AZ430288/c

LOCUS AZ430288 23 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0214012R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0214012 R, DNA sequence.

ACCESSION AZ430288
 VERSION AZ430288.1 GI:10554301
 KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

84112, USA

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0214 row: 0 column: 12
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source

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1..23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0214012"
/cclone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1147321141gblAFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Db 23 AGAGAGAGAGAGAGAG 6

RESULT 13
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 DEFINITION 2M0096G06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0096G06 R, DNA sequence.

ACCESSION AZ822888
 VERSION AZ822888.1 GI:12992796
 KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

84112, USA

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
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 Seq primer: CACAGAGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone="UUC2M0248N15"
 /clone_lib="Mouse 10kb plasmid UUC2M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil47321141gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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 Db 2 AGAGAGAGAGAGAGAG 19

RESULT 14

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 DEFINITION 2M0248N15F Mouse 10kb plasmid UUC2M library Mus musculus genomic clone UUC2M0248N15 F, DNA sequence.

ACCESSION AZ973926
 VERSION 1
 KEYWORDS GI:13845153
 SOURCE GSS.

ORGANISM house mouse.
 Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunne@genetics.utah.edu
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 Seq primer: CGTTGTAACACGAGCCGACGT
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 High quality sequence stop: 23.
 Location/Qualifiers
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 /clone="UUC2M0248N15"
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BASE COUNT 1 a 11 c 1 g 10 t
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Query Match 100.0%; Score 18; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagagagagagagagag 18
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 Db 22 AGAGAGAGAGAGAGAG 5

RESULT 15

AZ389918/c
 LOCUS 25 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0151E05F Mouse 10kb plasmid UUC2M library Mus musculus genomic clone UUC2M0151E05 F, DNA sequence.

ACCESSION AZ389918
 VERSION 1
 KEYWORDS GI:10503626
 SOURCE GSS.

ORGANISM house mouse.
 Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 25)

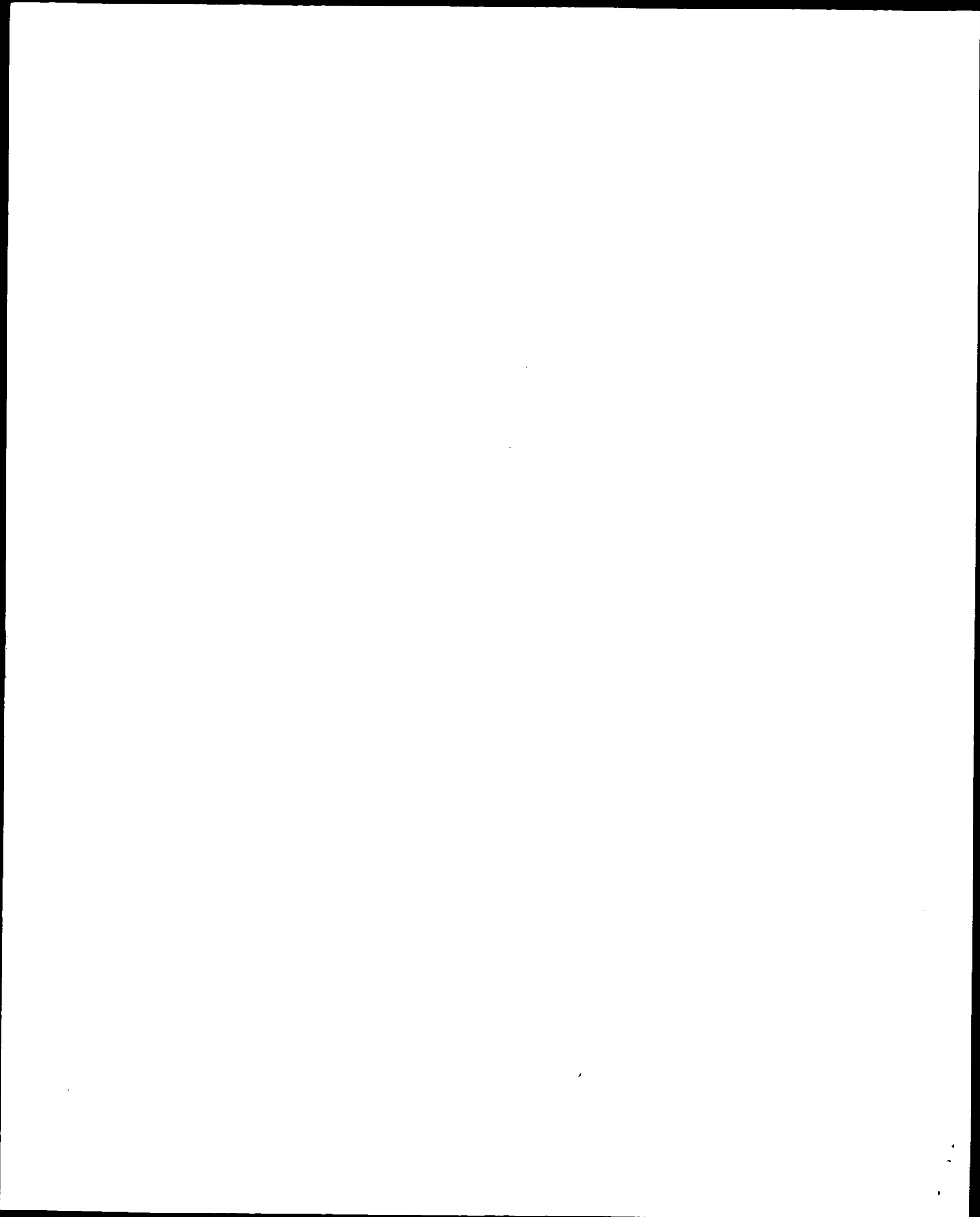
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606




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DEFINITION Sequence 25 from Patent WO9924578.
ACCESSION A95992
VERSION A95992.1 GI:6779888
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 25 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
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Db 1 n 1

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DEFINITION Sequence 35 from Patent WO9924578.
ACCESSION A96002
VERSION A96002.1 GI:6779893
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 35 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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ACCESSION A96002
VERSION A96002.1 GI:6779893
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 35 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
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/db_xref="taxon:32644"
BASE COUNT 0 a 0 c 0 g 0 t 1 others
ORIGIN

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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 n 1

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DEFINITION Sequence 45 from Patent WO9924578.
ACCESSION A96012
VERSION A96012.1 GI:6779898
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1)
AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 45 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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Db 1 n 1

RESULT 6
LOCUS A96012/c A96012 1 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 45 from Patent WO9924578.

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AUTHORS	Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE	Neisserial antigens
JOURNAL	Patent: WO 9924578-A 55 20-MAY-1999;
	PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
	CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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VERSION	A96040.1 GI:6779912
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ORGANISM	unidentified
REFERENCE	1 (bases 1 to 1)
AUTHORS	Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE	Neisserial antigens
JOURNAL	Patent: WO 9924578-A 73 20-MAY-1999;
	PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
	CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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ACCESSION	A96040
VERSION	A96040.1 GI:6779912
KEYWORDS	.
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ORGANISM	unidentified
REFERENCE	1 (bases 1 to 1)
AUTHORS	Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
TITLE	Neisserial antigens
JOURNAL	Patent: WO 9924578-A 73 20-MAY-1999;
	PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
	CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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 KEYWORDS
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 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 924578-A 91 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

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LOCUS A96058 A96058 1 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 91 from Patent WO924578.
 ACCESSION A96058
 VERSION A96058.1 GI:6779921
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 924578-A 91 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

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 ACCESSION A96076
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 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 924578-A 109 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

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 ACCESSION A96076
 VERSION A96076.1 GI:6779930
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 924578-A 109 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

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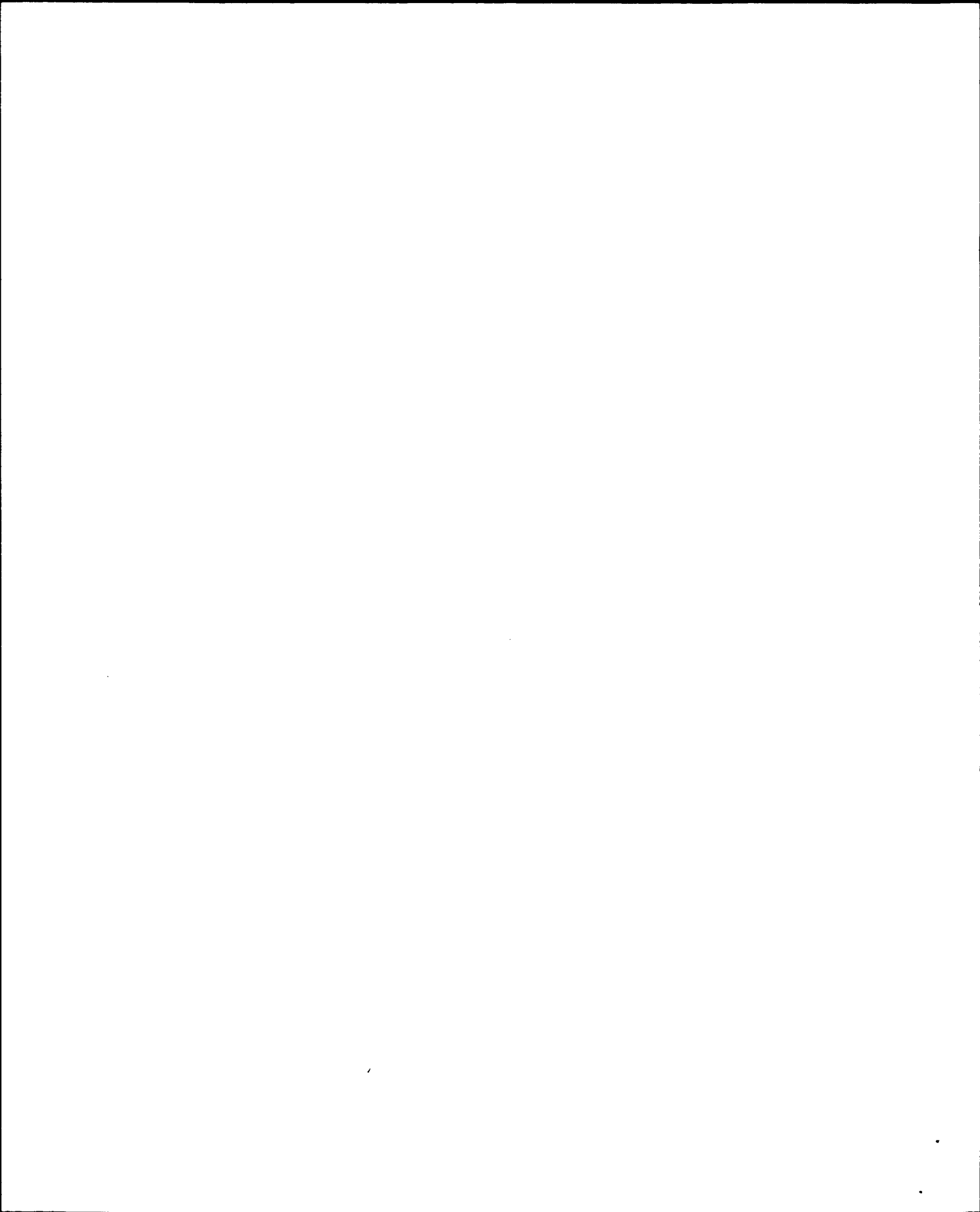
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 ORGANISM unidentified.
 unclassified.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 9924578-A 119 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
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GenCore version 4.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C	12	0	0.0	3	22	AA120244	Human breast cance
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C	17	0	0.0	4	18	AAT86385	Probe for target n
C	18	0	0.0	4	18	AAT86385	Probe for target n
C	19	0	0.0	4	18	AAT77252	Immunostimulatory
C	20	0	0.0	4	18	AAT77252	Immunostimulatory
C	21	0	0.0	4	22	AA117191	Human breast cance
C	22	0	0.0	4	22	AA117191	Human breast cance
C	23	0	0.0	4	22	AA124357	Human breast cance
C	24	0	0.0	4	22	AA124357	Human breast cance
C	25	0	0.0	4	22	AA124357	Human breast cance
C	26	0	0.0	4	22	AA124357	Human breast cance
C	27	0	0.0	4	22	AA124357	Human breast cance
C	28	0	0.0	5	10	AA93676	Cyclin binding ham
C	29	0	0.0	5	10	AA93676	Cyclin binding ham
C	30	0	0.0	5	15	AAQ68752	Synthetic probe fo
C	31	0	0.0	5	15	AAQ68752	Synthetic probe fo
C	32	0	0.0	5	16	AAQ81667	CH255 heavy chain
C	33	0	0.0	5	16	AAQ81667	CH255 heavy chain
C	34	0	0.0	5	16	AAQ81667	brGF binding oligo
C	35	0	0.0	5	16	AAQ81666	brGF binding oligo
C	36	0	0.0	5	17	AAT12043	brGF binding oligo
C	37	0	0.0	5	17	AAT12043	Cleavable replicab
C	38	0	0.0	5	19	AAV61663	Fusarium sp. 18S r
C	39	0	0.0	5	19	AAV61663	Fusarium sp. 18S r
C	40	0	0.0	5	19	AAT96299	Fungal telomeric n
C	41	0	0.0	5	20	AA210695	Fungal telomeric n
C	42	0	0.0	5	20	AA210695	Oligonucleotide se
C	43	0	0.0	5	20	AA210696	Oligonucleotide se
C	44	0	0.0	5	20	AA210696	Oligonucleotide se
C	45	0	0.0	5	20	AA211611	DNA enhancer seque

ALIGNMENTS

RESULT 1
AA57131
ID AA57131 standard; DNA; 1 BP.

XX AA57131;

DT 22-JUL-1999 (first entry)

XX Human mutant KCNQ3 primer 26.

DE KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;

XX Benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;

KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;

KW detection; gene therapy; drug screening; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9921875-A1.

XX 06-MAY-1999.

XX 23-OCT-1998; 98WO-US22375.

XX 24-OCT-1997; 97US-0063147.

XX (UTAH) UNIV UTAH RES FOUND.

XX Charlier C, Leppert MF, Singh NA;

XX WPI; 1999-312938/26.

PT Nucleic acid encoding potassium channels KCNQ2 and 3
 XX Claim 65; Page 151; 195pp; English.

CC This invention describes novel human and mouse potassium channel
 CC proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode
 CC KCNQ2 or KCNQ3, or the loss of one copy of these genes is used for
 CC diagnosis and prognosis of benign familial neonatal epilepsy (BFNE),
 CC juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or
 CC transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the
 CC proteins themselves in cell-free form) are used to screen for agents that
 CC can be used to treat or prevent these forms of epilepsy. Fragments of the
 CC encoding nucleic acids are used as probes or primers, either for
 CC detecting mutations or for isolation of related sequences, while the
 CC complete sequences may be used in gene therapy to provide wild-type
 CC protein. Antibodies specific for mutant or wild-type proteins are used
 CC as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins
 CC are useful in rational design of drugs and therapeutically (in
 CC replacement therapies). The forms of epilepsy associated with mutations
 CC in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are
 CC manifest), and better treatment options will be available.
 CC AAX57074-X57139 are primers used in the method of the invention.

XX Sequence 1 BP; 1 A; 0 C; 0 G; 0 U; 0 other;

Query Match 0.0%; Score 0; DB 20; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1
 Db 1 a 1

RESULT 2
 AAX57131/C
 ID AAX57131 standard; DNA; 1 BP.

XX AAX57131;

DT 22-JUL-1999 (first entry)

DE Human mutant KCNQ3 primer 26.

XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
 KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
 KW detection; gene therapy; drug screening; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9921875-A1.

XX 06-MAY-1999.

XX 23-OCT-1998; 98WO-US22375.

XX 24-OCT-1997; 97US-0063147.

XX (UTAH) UNIV UTAH RES FOUND.

XX Charlier C, Leppert MF, Singh NA;

XX WPI; 1999-312938/26.

XX Nucleic acid encoding potassium channels KCNQ2 and 3

XX Claim 65; Page 151; 195pp; English.

XX This invention describes novel human and mouse potassium channel
 CC proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode

CC KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for
 CC diagnosis and prognosis of benign familial neonatal epilepsy (BFNE),
 CC juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or
 CC transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the
 CC proteins themselves in cell-free form) are used to screen for agents that
 CC can be used to treat or prevent these forms of epilepsy. Fragments of the
 CC encoding nucleic acids are used as probes or primers, either for
 CC detecting mutations or for isolation of related sequences, while the
 CC complete sequences may be used in gene therapy to provide wild-type
 CC protein. Antibodies specific for mutant or wild-type proteins are used
 CC as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins
 CC are useful in rational design of drugs and therapeutically (in
 CC replacement therapies). The forms of epilepsy associated with mutations
 CC in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are
 CC manifest), and better treatment options will be available.
 CC AAX57074-X57139 are primers used in the method of the invention.

XX Sequence 1 BP; 1 A; 0 C; 0 G; 0 U; 0 other;

Query Match 0.0%; Score 0; DB 20; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 n 1

Db 1 T 1

RESULT 3

AAN80743
 ID AAN80743 standard; DNA; 3 BP.

XX AAN80743;

DT 10-SEP-1990 (first entry)

XX Sequence encoding complete mature and precursor forms of human tissue
 DE factor heavy chain proteins (hutfh & pre-hutfh, respectively).

XX Human tissue factor heavy chain (hutfh); immunoassays;
 KW precursor human tissue factor heavy chain (pre-hutfh);
 KW human tissue factor detection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 34..921

FT /tag= a

FT /product=pre-hutfh

FT mat_peptide 130..921

FT /tag= b

FT /product=hutfh

XX WO8807543-A.

XX 06-OCT-1988.

XX 29-MAR-1988; 88WO-US00998.

XX 25-JUN-1987; 87US-0067103.

XX (SCRI-) SCRIPPS CLINIC RES.

XX Eddington TS, Morrissey JH;

XX WPI; 1988-292837/41.

XX P-PSDB; AAP80713.

XX New DNA segment -

PT has gene encoding human tissue factor heavy chain protein and is
 PT useful for inhibiting coagulation

PS Disclosure; ; pp; English.

XX A DNA segment with a nucleotide sequence from about 130 to about 918 of
CC the sequence given here is claimed. Also claimed are antibodies which
CC immunoreact with hufFH and the claimed peptides (given in AAP80713).
CC The antibodies may be used in immunoassays for detection of hufFH. The
CC claimed peptides may be used to inhibit the binding of hufFH to
CC coagulation factor VII/VIIa in vivo.

XX Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 9; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1

Db 1 n 1

RESULT 4

AA080743/c

ID AA080743 standard; DNA; 3 BP.

XX AC AA080743;

XX DT 10-SEP-1990 (first entry)

XX DE Sequence encoding complete mature and precursor forms of human tissue
DE factor heavy chain proteins (hufFH & pre-hufFH, respectively).

XX KW Human tissue factor heavy chain (hufFH); immunoassays;

XX KW precursor human tissue factor heavy chain (pre-hufFH);

XX KW human tissue factor detection.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 34..921

XX FT /*tag= a

XX FT /product=pre-hufFH

XX FT mat_peptide 130..921

XX FT /*tag= b

XX FT /product=hufFH

XX PN W08807543-A.

XX PD 06-OCT-1988.

XX PF 29-MAR-1988; 88WO-US00998.

XX PR 25-JUN-1987; 87US-0067103.

XX PA (SCRI-) SCRIPPS CLINIC RES.

XX PI Eddington TS, Morrissey JH;

XX DR WPI: 1988-292837/41.

XX DR P-PSDB; AAP80713.

XX PT New DNA segment -
PT has gene encoding human tissue factor heavy chain protein and is
PT useful for inhibiting coagulation

XX PS Disclosure; ; pp; English.

XX A DNA segment with a nucleotide sequence from about 130 to about 918 of
CC the sequence given here is claimed. Also claimed are antibodies which
CC immunoreact with hufFH and the claimed peptides (given in AAP80713).
CC The antibodies may be used in immunoassays for detection of hufFH. The
CC claimed peptides may be used to inhibit the binding of hufFH to
CC coagulation factor VII/VIIa in vivo.

XX SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 9; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1

Db 3 N 3

RESULT 5

AA085491

ID AA085491 standard; CDNA; 3 BP.

XX AC AA085491;

XX DT 18-AUG-1995 (first entry)

XX DE Plasmid pEZZ318.thy2.

XX KW OMTKY3: turkey ovomucoid third domain peptide inhibitor;

XX KW furin inhibitor; protease inhibitor; pEZZ318.thy2; probe;

XX KW Escherichia coli; ss.

XX OS Synthetic.

XX PN W09502055-A.

XX PD 19-JAN-1995.

XX PF 08-JUL-1994; 94WO-US07779.

XX PR 09-JUL-1993; 93US-0089248.

XX PA (ANDE/) ANDERSON S.

XX PA (LASK/) LASKOWSKI M.

XX PI Anderson S, Laskowski M;

XX DR WPI: 1995-066900/09.

XX PT Protein inhibitors of serine proteinase(s), e.g. furin, deriv.
PT from turkey ovomucoid third domain - used as laboratory reagents
PT to study the proteinase(s), or as chemotherapeutic agents to
PT treat diseases associated with them

XX PS Disclosure; Page 42-45; 66pp; English.

XX CC In synthetic analogs of turkey ovomucoid domain protein (6-56)
CC (OMTKY3), given in AAR69818-24, the region immediately adjacent to
CC the reactive site peptide bond is mutated to include the consensus
CC sequence of furin or other serine protease. Polynucleotides
CC encoding such analogs are incorporated into pEZZ318.thy2 and
CC expressed in Escherichia coli RV308 (ATCC 31608).

XX SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 3 other;

Query Match 0.0%; Score 0; DB 16; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 n 1

Db 1 n 1

RESULT 6

AA085491/c

ID AA085491 standard; CDNA; 3 BP.

The present invention relates to human and murine cDNAs from a neurosensory defect associated gene family. The novel cDNAs are mouse tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB form 6 (see AAA94632), human TUB form I (see AAA94633), human TULP1 (see AAA94633), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and mouse TULP4 (see AAA94638). The novel coding sequences are useful as immunogens to raise antibodies that specifically identify TUB/TULP expressing cells and in drug screening assays directed at neurosensory defects. The novel proteins encoded by the present sequence can be used for the treatment of neurosensory degenerative conditions e.g. retinal dystrophies. The present sequence is a probe used to isolate the novel

Query Match 0.0%; Score 0; DB 21; Length 3;

```

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 3 C 3

RESULT 11
AAL20244
ID AAL20244 standard; cDNA; 3 BP.
XX
AC AAL20244;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 12701.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
XX
PR 14-MAR-2000; 2000US-0189167.
XX
PR 24-MAR-2000; 2000US-0192099.
XX
PR 29-MAR-2000; 2000US-0193480.
XX
PR 15-MAY-2000; 2000US-0205230.
XX
PR 09-JUN-2000; 2000US-0211315.
XX
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI; 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer
PS Claim 1; Page 2245; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

Query Match 0.0%; Score 0; DB 22; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 3 A 3

RESULT 13
AAL081664
ID AAQ81664 standard; RNA; 4 BP.
XX
AC AAQ81664;
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #1.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO9500528-A.

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XX PD 05-JAN-1995.
XX XX
XX PF 17-JUN-1994; 94WO-US06884.
XX XX
XX PR 18-JUN-1993; 93US-0079677.
XX PR 07-JAN-1994; 94US-0179491.
XX XX
XX PA (PHAR-) PHARMAGENICS INC.
XX XX
XX PI Beutel BA, Joesten ME;
XX XX
XX DR WPI; 1995-051992/07.
XX XX
XX XX New oligo-nucleotide(s) that bind to basic fibroblast growth
XX PT factor - modulating, esp. inhibiting, its activity, useful in
XX PT treating cancer, preventing metastasis, and diagnosis.
XX XX
XX PS Claim 3; Page 25; 44pp; English.
XX XX
XX CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
XX CC the activity of basic fibroblast growth factor (bFGF) by binding
XX CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67
XX CC represent core sequences of which at least one is present in each of
XX CC the binding oligos. These oligonucleotides may form a single
XX CC strand, double strand, a stem-loop structure, a bubble structure, a
XX CC pseudoknot or a closed, circular structure. bFGF binds to high
XX CC affinity receptor and low affinity heparin-like molecules on the
XX CC cell surface. These oligonucleotides bind to bFGF in competition
XX CC with its receptor and heparin. These oligonucleotides may inhibit
XX CC or enhance the activity of bFGF. Particularly, they inhibit
XX CC neovascularisation so they can be used to suppress growth of solid
XX CC tumours and to reduce the risk of metastasis. They can be used as
XX CC diagnostic reagents to determine the presence of thrombin, or used in
XX CC gene therapy.
XX SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 16; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 g 1

RESULT 14
AAQ81664/c
ID AAQ81664 standard; RNA; 4 BP.
XX AC AAQ81664;
XX XX
XX DT 29-SEP-1995 (first entry)
XX XX
XX DE bFGF binding oligomer core sequence #1.
XX XX
XX KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
XX KW bubble structure; pseudoknot; receptor; heparin; competition;
XX KW inhibition; enhance; neovascularisation; solid tumour; cancer;
XX KW metastasis; diagnosis; gene therapy; ss.
XX OS Synthetic.
XX XX
XX PN WO9500528-A.
XX XX
XX PD 05-JAN-1995.
XX XX
XX PF 17-JUN-1994; 94WO-US06884.
XX XX
XX PR 18-JUN-1993; 93US-0079677.
XX PR 07-JAN-1994; 94US-0179491.
XX XX
XX PA (PHAR-) PHARMAGENICS INC.
XX PI Beutel BA, Joesten ME;
XX PI WPI; 1995-051992/07.
XX DR

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XX PA (PHAR-) PHARMAGENICS INC.
XX XX
XX PI Beutel BA, Joesten ME;
XX XX
XX DR WPI; 1995-051992/07.
XX XX
XX XX New oligo-nucleotide(s) that bind to basic fibroblast growth
XX PT factor - modulating, esp. inhibiting, its activity, useful in
XX PT treating cancer, preventing metastasis, and diagnosis.
XX XX
XX PS Claim 3; Page 25; 44pp; English.
XX XX
XX CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
XX CC the activity of basic fibroblast growth factor (bFGF) by binding
XX CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67
XX CC represent core sequences of which at least one is present in each of
XX CC the binding oligos. These oligonucleotides may form a single
XX CC strand, double strand, a stem-loop structure, a bubble structure, a
XX CC pseudoknot or a closed, circular structure. bFGF binds to high
XX CC affinity receptor and low affinity heparin-like molecules on the
XX CC cell surface. These oligonucleotides bind to bFGF in competition
XX CC with its receptor and heparin. These oligonucleotides may inhibit
XX CC or enhance the activity of bFGF. Particularly, they inhibit
XX CC neovascularisation so they can be used to suppress growth of solid
XX CC tumours and to reduce the risk of metastasis. They can be used as
XX CC diagnostic reagents to determine the presence of thrombin, or used in
XX CC gene therapy.
XX SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 16; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 4 G 4

RESULT 15
AAQ81665
ID AAQ81665 standard; RNA; 4 BP.
XX AC AAQ81665;
XX XX
XX DT 29-SEP-1995 (first entry)
XX XX
XX DE bFGF binding oligomer core sequence #2.
XX XX
XX KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
XX KW bubble structure; pseudoknot; receptor; heparin; competition;
XX KW inhibition; enhance; neovascularisation; solid tumour; cancer;
XX KW metastasis; diagnosis; gene therapy; ss.
XX OS Synthetic.
XX XX
XX PN WO9500528-A.
XX XX
XX PD 05-JAN-1995.
XX XX
XX PF 17-JUN-1994; 94WO-US06884.
XX XX
XX PR 18-JUN-1993; 93US-0079677.
XX PR 07-JAN-1994; 94US-0179491.
XX XX
XX PA (PHAR-) PHARMAGENICS INC.
XX PI Beutel BA, Joesten ME;
XX PI WPI; 1995-051992/07.
XX DR

```

PT New oligo-nucleotide(s) that bind to basic fibroblast growth
PT factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.
XX
XX
PS Claim 3; Page 25; 44pp; English.
XX
CC The sequences given in AA081642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AA081664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
XX gene therapy.
XX
SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 0.0%; Score 0; DB 16; Length 4;
Best Local Similarity 0.0%; Pred. NO. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 c 1

Search completed: August 24, 2002, 22:08:17
Job time: 8850 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 21:57:39 ; Search time 159.68 Seconds
(without alignments)
27.689 Million cell updates/sec

Title: US-10-077-383-33
Perfect score: 18
Sequence: 1 nnnnnnnnnnnnnnnnn 18

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries:

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4: /cgn2.6/ptodata/2/ina/!B_COMB.seq.*
5: /cgn2.6/ptodata/2/ina/!CTUS_COMB.seq.*
6: /cgn2.6/ptodata/2/ina/!hackfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	0	0.0	2	1	US-08-268-6798-8
5	0	0.0	2	1	US-08-457-274A-16
6	0	0.0	2	1	US-08-457-274A-16
7	0	0.0	2	1	US-08-484-192-16
8	0	0.0	2	1	US-08-484-192-16
9	0	0.0	2	2	US-08-726-464B-28
10	0	0.0	2	2	US-08-726-464B-28
11	0	0.0	2	3	US-09-016-520-35
12	0	0.0	2	3	US-09-016-520-35
13	0	0.0	2	4	US-09-130-973-35
14	0	0.0	2	4	US-09-130-973-35
15	0	0.0	2	4	US-09-477-902-35
16	0	0.0	2	4	US-09-477-902-35
17	0	0.0	2	4	US-08-361-024-3
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21	0	0.0	2	4	US-09-411-862A-16
22	0	0.0	2	4	US-09-411-862A-16
23	0	0.0	2	5	PCT-US95-C5758-16
24	0	0.0	2	5	PCT-US95-C5758-16
25	0	0.0	3	1	US-07-791-213D-46
26	0	0.0	3	1	US-07-791-213D-46
27	0	0.0	3	1	US-07-791-213D-62

c	28	0	0.0	3	1	US-07-791-213D-62	Sequence 62, Appl
c	29	0	0.0	3	1	US-08-268-6798-7	Sequence 7, Appl
c	30	0	0.0	3	1	US-08-268-6798-7	Sequence 7, Appl
c	31	0	0.0	3	1	US-08-268-6798-7	Sequence 22, Appl
c	32	0	0.0	3	1	US-08-295-743-22	Sequence 2, Appl
c	33	0	0.0	3	1	US-08-295-743-22	Sequence 2, Appl
c	34	0	0.0	3	1	US-08-602-036A-2	Sequence 46, Appl
c	35	0	0.0	3	1	US-08-602-036A-2	Sequence 46, Appl
c	36	0	0.0	3	1	US-08-293-150A-46	Sequence 62, Appl
c	37	0	0.0	3	1	US-08-293-150A-46	Sequence 62, Appl
c	38	0	0.0	3	1	US-08-293-150A-62	Sequence 2, Appl
c	39	0	0.0	3	2	US-08-502-374A-2	Sequence 2, Appl
c	40	0	0.0	3	2	US-08-502-374A-2	Sequence 2, Appl
c	41	0	0.0	3	2	US-08-502-374A-2	Sequence 2, Appl
c	42	0	0.0	3	2	US-08-642-407A-2	Sequence 2, Appl
c	43	0	0.0	3	3	US-08-873-709-9	Sequence 9, Appl
c	44	0	0.0	3	3	US-08-873-709-9	Sequence 9, Appl
c	45	0	0.0	3	3	US-09-032-365A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
PCT-US93-00977-702
; Sequence 702, Application PC/TUS9300977
; GENERAL INFORMATION:
; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
; NUMBER OF SEQUENCES: 711
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson, and Bear
; STREET: 620 Newport Center Dr. Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00977
; FILING DATE: 19930129
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: HITACHI.006H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 702:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-00977-702

Query Match 0.08; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 A 1

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RESULT 2
PCT-US93-00977-702/c
; Sequence 702, Application PC/TUS9300977
; GENERAL INFORMATION:
; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
; NUMBER OF SEQUENCES: 711
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobber, Martens, Olson, and Bear
; STREET: 620 Newport Center Dr. Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00977
; FILING DATE: 19930129
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: HITACHI.006H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 702:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-00977-702

```

```

Query Match 0.0%; Score 0; DB 5; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy 1 n 1
Db 1 T 1

```

```

RESULT 3
US-08-268-679B-8
; Sequence 8, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD; MOLLA,
; APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/268,679B
; FILING DATE: 30-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07\846,914
; FILING DATE: 06-MAR-1992
; CLASSIFICATION: 435
; APPLICATION NUMBER: 07\719,761
; FILING DATE: 24-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MARIA C.H. LIN
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 0887-4095 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEEX: 421792
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: OLIGONUCLEOTIDE
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE: N.A.
; POSITION IN GENOME: N.A.
US-08-268-679B-8

```

```

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 n 1
Db 1 G 1

```

```

RESULT 4
US-08-268-679B-8/c
; Sequence 8, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD; MOLLA,
; APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,679B
; FILING DATE: 30-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07\846,914
; FILING DATE: 06-MAR-1992
; CLASSIFICATION: 435
; APPLICATION NUMBER: 07\719,761
; FILING DATE: 24-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MARIA C.H. LIN

```

; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 0887-4095 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: OLIGONUCLEOTIDE
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE: N.A.
; POSITION IN GENOME: N.A.
; US-08-268-679B-8

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 2 C 2

RESULT 5
US-08-457-274A-16
; Sequence 16, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; APPLICANT: Tomita, Takashi
; TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Musca domestica
; STRAIN: Learn-Pyr
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
; US-08-457-274A-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 2 T 2

; STRAIN: Learn-Pyr
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
; US-08-457-274A-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 1 A 1

RESULT 6
US-08-457-274A-16/c
; Sequence 16, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; APPLICANT: Tomita, Takashi
; TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Musca domestica
; STRAIN: Learn-Pyr
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
; US-08-457-274A-16

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 n 1
Db 2 T 2

RESULT 7

```

US-08-484-192-16
; Sequence 16, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1,"")
; OTHER INFORMATION: /note= "This is a biotin-17
; OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-484-192-16

```

```

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 n 1
Db 1 N 1

```

RESULT 8

```

US-08-484-192-16/c
; Sequence 16, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN

```

```

; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1,"")
; OTHER INFORMATION: /note= "This is a biotin-17
; OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-484-192-16

```

```

Query Match 0.0%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 n 1
Db 2 C 2

```

RESULT 9

```

US-08-726-464B-28
; Sequence 28, Application US/08726464B
; Patent No. 5932546
; GENERAL INFORMATION:
; APPLICANT: BARRETT, Ronald W.
; APPLICANT: DOWER, William J.
; APPLICANT: CWIRLA, Steven A.
; APPLICANT: JOHNSON, Sherril S.
; APPLICANT: WRIGHTON, Nicholas C.
; APPLICANT: DUFFIN, David J.
; APPLICANT: WAGSTROM, Christopher R.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO THE
; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:

```



```

; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,464B
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-024100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/576-0300
; TELEFAX: 415/576-0300
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; US-08-726-464B-28

```

```

Query Match          0.0%; Score 0; DB 2; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 n 1
Db 1 v 1

```

```

RESULT 10
US-08-726-464B-28/c
; Sequence 28, Application US/08726464B
; Patent No. 5932546
; GENERAL INFORMATION:
; APPLICANT: BARRETT, Ronald W.
; APPLICANT: DOWER, William J.
; APPLICANT: COWLA, Steven A.
; APPLICANT: JOHNSON, Sherril S.
; APPLICANT: WRIGHTON, Nicholas C.
; APPLICANT: DUFFIN, David J.
; APPLICANT: WAGSTROM, Christopher R.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO THE
; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,464B
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-024100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/576-0200
; TELEFAX: 415/576-0300
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; US-08-726-464B-28

```

```

Query Match          0.0%; Score 0; DB 2; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 n 1
Db 2 y 2

```

```

RESULT 11
US-09-016-520-35
; Sequence 35, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
; US-09-016-520-35

```

```

Query Match          0.0%; Score 0; DB 3; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 n 1
Db 1 t 1

```

```

RESULT 12
US-09-016-520-35/c
; Sequence 35, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides

```

```

; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-35

```

```

Query Match          0.0%; Score 0; DB 3; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 n 1
Db 2 A 2

```

```

RESULT 13
US-09-130-973-35
; Sequence 35, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
US-09-130-973-35

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 n 1
Db 1 t 1

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RESULT 14
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; Sequence 35, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:

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; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
US-09-130-973-35

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RESULT 15
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; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
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US-09-477-902-35

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Qy 1 n 1
Db 1 t 1

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Mon Aug 26 10:18:21 2002

us-10-077-383-33.rni

Page 7

Search completed: August 24, 2002, 21:57:39
Job time: 21597 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2002, 21:19:26 ; Search time 4810.92 Seconds
(without alignments)
50.499 Million cell updates/sec

Title: US-10-077-383-33

Perfect score: 18

Sequence: 1 nnnnnnnnnnnnnnnnn 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: em_estba:*
- 2: em_estba:*
- 3: em_estin:*
- 4: em_estin:*
- 5: em_estm:*
- 6: em_estov:*
- 7: em_estpl:*
- 8: em_estro:*
- 9: em_hic:*
- 10: gb_est1:*
- 11: gb_hic:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	0	0.0	1	2	HS0001740	AL037411 Homo sapi
3	0	0.0	1	2	HS0003869	AL039393 Homo sapi
4	0	0.0	1	2	HS0003869	AL039393 Homo sapi
5	0	0.0	1	2	HS0005008	AL040532 Homo sapi
6	0	0.0	1	2	HS0005008	AL040532 Homo sapi
7	0	0.0	1	2	HS0011115	AL046265 Homo sapi
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9	0	0.0	1	2	HS0011270	AL046420 Homo sapi
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ALIGNMENTS

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XX AL037411.1

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DT 12-WAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp564L2071_s1 (from clone DKFZp564L2071)

DE EST; expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RP 1-1

RT Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;

RL Submitted (12-WAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by GBF within the cDNA

CC sequencing consortium of the German Genome Project

CC No r1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..1

FT /db_xref="taxon:9606"

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FT /clone="DKFZp564L2071"

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Db      1 C 1

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SV      AL037411.1
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DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
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DE      Homo sapiens mRNA; EST DKFZp564L2071_s1 (from clone DKFZp564L2071)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
[1]
RN      1-1
RA      Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by GBF within the cDNA
CC      sequencing consortium of the German Genome Project
CC      NO r1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 G 1

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SV      AL039393.1
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DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
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XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
[1]
RN      1-1
RA      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC      sequencing consortium of the German Genome Project
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
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Db      1 A 1

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DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
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XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.

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RP 1-1
RA Duisterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
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FT DH10B; sites NotI + SalI"
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FT /tissue_type="testis"
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
Db 1 T 1

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XX SV AL040532.1
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DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
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KW EST; expressed sequence tag.
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OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
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RP 1-1
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BNFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
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Db 1 T 1

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XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
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RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
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RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
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CC Clone from S. Wiemann, sequenced by BNFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers

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Db 1 C 1

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DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
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XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
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RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BNFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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KW      EST; expressed sequence tag.
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OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-1
RA      Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT      ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
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CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
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Db      1 G 1

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SV      AL046265.1
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DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
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KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RP      1-1
RA      Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT      ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
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CC      Clone from S. Wiemann, sequenced by BMFZ within the cdna
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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Db      1 C 1

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ID      HSM011270 standard; RNA; EST; 1 BP.
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AC      AL046420;
XX
SV      AL046420.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434N037_r1 (from clone DKFZp434N037)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-1
RA      Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT      ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by BMFZ within the cdna
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin

```


CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers
 FH source
 FT 1..1
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434N037"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
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Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 C 1

RESULT 10
 HSM011270/c
 ID HSM011270 standard; RNA; EST; 1 BP.
 XX
 XX AL046420.1
 XX AL046420.1
 DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 XX Homo sapiens mRNA; EST DKFZp434N037_r1 (from clone DKFZp434N037)
 XX
 XX EST; expressed sequence tag.

OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]
 RN 1-1
 RP Koehler K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
 XX

CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No s1 sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers
 FH source
 FT 1..1
 FT /db_xref="taxon:9606"
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 FT /clone="DKFZp434N037"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 XX Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Qy 1 n 1
 Db 1 C 1

Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 G 1

RESULT 11
 HSM011922
 ID HSM011922 standard; RNA; EST; 1 BP.
 XX
 XX AL047072;
 XX AL047072.1

XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 XX Homo sapiens mRNA; EST DKFZp586P0817_r1 (from clone DKFZp586P0817)
 XX
 XX EST; expressed sequence tag.

OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]
 RN 1-1
 RP Koehler K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No s1 sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers
 FH source
 FT 1..1
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp586P0817"
 FT /clone_lib="586 (synonym: htel). Vector pSport1; host
 FT DH10B; sites NotI + SalI/MluI"
 FT /dev_stage="adult"
 FT /tissue_type="uterus"
 XX

SQ Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;

Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1
 Db 1 C 1

RESULT 12
 HSM011922/c
 ID HSM011922 standard; RNA; EST; 1 BP.
 XX
 XX AL047072;
 XX AL047072.1

DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 DE Homo sapiens mRNA; EST DKFZp586P0817_r1 (from clone DKFZp586P0817)
 KW EST; expressed sequence tag.
 XX
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX
 RN [1]
 RP 1-1
 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No sl sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de
 XX
 FH Key Location/Qualifiers
 FT source 1. .1
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp586P0817"
 FT /clone_lib="586 (synonym: hute1). Vector pSport1; host
 FT DH10B; sites NotI + SalI/MluI"
 FT /dev_stage="adult"
 FT /tissue_type="uterus"
 XX
 SQ Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 other;
 Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 n 1
 DB 1 G 1
 RESULT 13
 BI416880 1 bp mRNA linear EST 15-AUG-2001
 LOCUS hasp002xj20f Heterobasidion annosum - Scots pine infection stage
 DEFINITION subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
 annosum cDNA clone hasp002xj20f, mRNA sequence.
 ACCESSION BI416880
 VERSION BI416880.1 GI:15187903
 KEYWORDS EST
 SOURCE Pinus sylvestris/Heterobasidion annosum.
 ORGANISM Pinus sylvestris/Heterobasidion annosum.
 Eukaryota; mixed EST libraries.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
 TITLE Expressed sequence tags of randomly selected cDNA clones from the
 interaction of the root rot fungus (Heterobasidion annosum) with
 seedling roots of Scots pine (Pinus sylvestris)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Fred O. Asiegbu
 Dept. of Forest Mycology & Pathology
 Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,
 Sweden
 Tel: +46 18 67 15 98
 Fax: +46 18 30 92 45
 Email: Fred.Asiegbu@mykopat.slu.se
 Seq primer: T7 primer.
 Location/Qualifiers
 1. .1
 /organism="Pinus sylvestris/Heterobasidion annosum"
 /db_xref="taxon:163015"
 /clone="hasp002xj20f"
 /clone_lib="Heterobasidion annosum - Scots pine infection
 stage subtraction cDNA library (hasp)"
 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
 hybridization cDNA library was constructed from scots
 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (FP5)."
 BASE COUNT 0 a 0 c 0 g 0 t 1 others
 ORIGIN

Seq primer: T7 primer.
 Location/Qualifiers
 1. .1
 /organism="Pinus sylvestris/Heterobasidion annosum"
 /db_xref="taxon:163015"
 /clone="hasp002xj20f"
 /clone_lib="Heterobasidion annosum - Scots pine infection
 stage subtraction cDNA library (hasp)"
 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
 hybridization cDNA library was constructed from scots
 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (FP5)."
 BASE COUNT 0 a 0 c 0 g 0 t 1 others
 ORIGIN

Query Match 0.0%; Score 0; DB 10; Length 1;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 n 1
 DB 1 n 1
 RESULT 14
 BI416880/c 1 bp mRNA linear EST 15-AUG-2001
 LOCUS hasp002xj20f Heterobasidion annosum - Scots pine infection stage
 DEFINITION subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
 annosum cDNA clone hasp002xj20f, mRNA sequence.
 ACCESSION BI416880
 VERSION BI416880.1 GI:15187903
 KEYWORDS EST
 SOURCE Pinus sylvestris/Heterobasidion annosum.
 ORGANISM Pinus sylvestris/Heterobasidion annosum.
 Eukaryota; mixed EST libraries.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
 TITLE Expressed sequence tags of randomly selected cDNA clones from the
 interaction of the root rot fungus (Heterobasidion annosum) with
 seedling roots of Scots pine (Pinus sylvestris)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Fred O. Asiegbu
 Dept. of Forest Mycology & Pathology
 Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,
 Sweden
 Tel: +46 18 67 15 98
 Fax: +46 18 30 92 45
 Email: Fred.Asiegbu@mykopat.slu.se
 Seq primer: T7 primer.
 Location/Qualifiers
 1. .1
 /organism="Pinus sylvestris/Heterobasidion annosum"
 /db_xref="taxon:163015"
 /clone="hasp002xj20f"
 /clone_lib="Heterobasidion annosum - Scots pine infection
 stage subtraction cDNA library (hasp)"
 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
 hybridization cDNA library was constructed from scots
 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (FP5)."
 BASE COUNT 0 a 0 c 0 g 0 t 1 others
 ORIGIN

Query Match 0.0%; Score 0; DB 10; Length 1;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 n 1
 DB 1 n 1
 RESULT 14
 BI416880/c 1 bp mRNA linear EST 15-AUG-2001
 LOCUS hasp002xj20f Heterobasidion annosum - Scots pine infection stage
 DEFINITION subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
 annosum cDNA clone hasp002xj20f, mRNA sequence.
 ACCESSION BI416880
 VERSION BI416880.1 GI:15187903
 KEYWORDS EST
 SOURCE Pinus sylvestris/Heterobasidion annosum.
 ORGANISM Pinus sylvestris/Heterobasidion annosum.
 Eukaryota; mixed EST libraries.
 REFERENCE 1 (bases 1 to 1)
 AUTHORS Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
 TITLE Expressed sequence tags of randomly selected cDNA clones from the
 interaction of the root rot fungus (Heterobasidion annosum) with
 seedling roots of Scots pine (Pinus sylvestris)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Fred O. Asiegbu
 Dept. of Forest Mycology & Pathology
 Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,
 Sweden
 Tel: +46 18 67 15 98
 Fax: +46 18 30 92 45
 Email: Fred.Asiegbu@mykopat.slu.se
 Seq primer: T7 primer.
 Location/Qualifiers
 1. .1
 /organism="Pinus sylvestris/Heterobasidion annosum"
 /db_xref="taxon:163015"
 /clone="hasp002xj20f"
 /clone_lib="Heterobasidion annosum - Scots pine infection
 stage subtraction cDNA library (hasp)"
 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
 hybridization cDNA library was constructed from scots
 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (FP5)."
 BASE COUNT 0 a 0 c 0 g 0 t 1 others
 ORIGIN

Qy 1 n 1
Db 1 N 1

RESULT 15

BI817896

LOCUS

BI817896 1 bp mRNA linear EST 04-OCT-2001
G3-023 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
to putative heterochromatin-like protein 1, mRNA sequence.

ACCESSION

BI817896

VERSION

BI817896.1

KEYWORDS

EST.

SOURCE

axolotl.

ORGANISM

Ambystoma mexicanum

REFERENCE

AUTHORS

Voss,S.R., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,
Gardiner,D.M. and Parichy,D.M.

TITLE

Expressed sequence tags from an axolotl limb regeneration library

JOURNAL

Unpublished (2001)

COMMENT

Contact: Voss SR

Department of Biology

Colorado State University

Fort Collins, CO 80523, USA

Tel: 970 491 4869

Fax: 970 491 0649

Email: srvoss@lamar.colostate.edu

Single pass sequence from 5' end. Low quality sequence was trimmed

from the ends (PHRED error rate = 5%). Trace file available:

srvoss@lamar.colostate.edu.

FEATURES

source

1..1

Location/Qualifiers

BASE COUNT

ORIGIN

0 a 1 c 0 g 0 t

/organism="Ambystoma mexicanum"

/db_xref="taxon:8296"

/clone_lib="Axolotl Lambda Zap Library"

/tissue_type="Regenerating forelimb"

/dev_stage="Medium-bud blastema"

Query Match

Best Local Similarity 0.0%; Score 0; DB 10; Length 1;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 n 1

Db 1 C 1

Search completed: August 24, 2002, 21:19:26

Job time: 20529 sec

